

MOR0251.ST25.txt
SEQUENCE LISTING

<110> Grasso, Luigi
Liang, Shaohong
Nicolaides, Nicholas C.
Sass, Philip M.

<120> METHODS OF GENERATING HIGH-PRODUCTION OF ANTIBODIES FROM
HYBRIDOMAS CREATED BY IN VITRO IMMUNIZATION

<130> MOR-0251

<150> US 60/427,165

<151> 2002-11-15

<150> US 60/501,650

<151> 2003-09-10

<160> 50

<170> PatentIn version 3.2

<210> 1

<211> 3063

<212> DNA

<213> Homo sapiens

<400> 1

```
ggcacgagtg gctgcttgcg gctagtggtat ggtaattgcc tgcctcgcg tagcagcaag      60
ctgctctgtt aaaagcgaaa atgaaacaat tgcctgcggc aacagttcga ctcttttcaa      120
gttctcagat catcacttcg gtggtcagtg ttgtaaaaga gcttattgaa aactccttgg      180
atgctggtgc cacaagcgta gatgttaaac tggagaacta tggatttgat aaaattgagg      240
tgcgagataa cggggagggt atcaaggctg ttgatgcacc tgtaatggca atgaagtact      300
acacctcaaa aataaatagt catgaagatc ttgaaaattt gacaacttac ggttttcgtg      360
gagaagcctt ggggtcaatt tgttgtatag ctgaggtttt aattacaaca agaacggctg      420
ctgataatth tagcaccag tatgttttag atggcagtg ccacatactt tctcagaaac      480
cttcacatct tgggtcaaggt acaactgtaa ctgctttaag attatttaag aatctacctg      540
taagaaagca gttttactca actgcaaaaa aatgtaaaga tgaaataaaa aagatccaag      600
atctcctcat gagctttggt atccttaaac ctgacttaag gattgtcttt gtacataaca      660
aggcagttat ttggcagaaa agcagagtat cagatcaca gatggctctc atgtcagttc      720
tggggactgc tggtatgaac aatatggaat cctttcagta ccactctgaa gaatctcaga      780
tttatctcag tggatttctt ccaaagtgtg atgcagacca ctctttcact agtctttcaa      840
caccagaaa agttttcatc ttcataaaca gtcgaccagt acatcaaaaa gatattctaa      900
agttaatccg acatcattac aatctgaaat gcctaaagga atctactcgt ttgtatcctg      960
ttttctttct gaaaatcgat gttcctacag ctgatgttga tgtaaattha acaccagata     1020
aaagccaagt attattacaa aataaggaat ctgttttaat tgctcttgaa aatctgatga     1080
cgacttgtha tggaccatta cctagtacaa attcttatga aaataataaa acagatgttt     1140
ccgcagctga catcgttctt agtaaaacag cagaaacaga tgtgcttttt aataaagtgg     1200
aatcatctgg aaagaattat tcaaatgttg atacttcagt cattccattc caaaatgata     1260
```

MOR0251.ST25.txt

tgcataatga tgaatctgga aaaaacactg atgattgttt aaatcaccag ataagtattg	1320
gtgacttttg ttatgggtcat tgtagtagtg aaattttctaa cattgataaa aacactaaga	1380
atgcatttca ggacatttca atgagtaatg tatcatggga gaactctcag acggaatata	1440
gtaaaacttg ttttataagt tccgttaagc acaccagtc agaaaatggc aataaagacc	1500
atatagatga gagggggaa aatgaggaag aagcagggtct tgaaaactct tcggaaattt	1560
ctgcagatga gtggagcagg ggaaatatac ttaaaaattc agtgggagag aatattgaac	1620
ctgtgaaaat tttagtgcct gaaaaaagtt taccatgtaa agtaagtaat aataattatc	1680
caatccctga acaaatgaat cttaatgaag attcatgtaa caaaaaatca aatgtaatag	1740
ataataaatc tggaaaagtt acagcttatg atttacttag caatcgagta atcaagaaac	1800
ccatgtcagc aagtgtctct tttgttcaag atcatcgtcc tcagtctctc atagaaaatc	1860
ctaagactag tttagaggat gcaacactac aaattgaaga actgtggaag acattgagt	1920
aagaggaaaa actgaaatat gaagagaagg ctactaaaga cttggaacga tacaatagtc	1980
aaatgaagag agccattgaa caggagtcac aaatgtcact aaaagatggc agaaaaaaga	2040
taaaaccac cagcgcagtg aatttggccc agaagcaca gttaaaaacc tcattatcta	2100
atcaaccaa acttgatgaa ctcttcagtc ccaaattga aaaaagaagg agtcaaaata	2160
ttaaaatggt acagatcccc ttttctatga aaaacttaaa aataaatttt aagaaacaaa	2220
acaaagtga cttagaagag aaggatgaac ctgtcttgat ccacaatctc aggtttcctg	2280
atgcatggct aatgacatcc aaaacagagg taatgttatt aaatccatat agagtagaag	2340
aagccctgct atttaaaaga cttcttgaga atcataaact tcctgcagag ccactggaaa	2400
agccaattat gttaacagag agtcttttta atggatctca ttatttagac gttttatata	2460
aaatgacagc agatgaccaa agatacagtg gatcaactta cctgtctgat cctcgtctta	2520
cagcgaatgg tttcaagata aaattgatac caggagtttc aattactgaa aattacttgg	2580
aaatagaagg aatggctaatt tgtctcccat tctatggagt agcagattta aaagaaattc	2640
ttaatgctat attaaacaga aatgcaaagg aagtttatga atgtagacct cgcaaagtga	2700
taagtatttt agagggagaa gcagtgcgtc tatccagaca attacccatg tacttatcaa	2760
aagaggacat ccaagacatt atctacagaa tgaagcacca gtttggaat gaaattaaag	2820
agtgtgttca tggctgcccc ttttttcac atttaaccta tcttccagaa actacatgat	2880
taaatatgtt taagaagatt agttaccatt gaaattgggt ctgtcataaa acagcatgag	2940
tctggtttta aattatcttt gtattatgtg tcacatgggt attttttaaa tgaggattca	3000
ctgacttgtt tttatattga aaaaagttcc acgtattgta gaaaacgtaa ataaactaat	3060
aac	3063

<210> 2
 <211> 932
 <212> PRT
 <213> Homo sapiens
 <400> 2

MOR0251.ST25.txt

Met Lys Gln Leu Pro Ala Ala Thr Val Arg Leu Leu Ser Ser Ser Gln
 1 5 10 15
 Ile Ile Thr Ser Val Val Ser Val Val Lys Glu Leu Ile Glu Asn Ser
 20 25 30
 Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys Leu Glu Asn Tyr Gly
 35 40 45
 Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val
 50 55 60
 Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser
 65 70 75 80
 His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala
 85 90 95
 Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr
 100 105 110
 Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His
 115 120 125
 Ile Leu Ser Gln Lys Pro Ser His Leu Gly Gln Gly Thr Thr Val Thr
 130 135 140
 Ala Leu Arg Leu Phe Lys Asn Leu Pro Val Arg Lys Gln Phe Tyr Ser
 145 150 155 160
 Thr Ala Lys Lys Cys Lys Asp Glu Ile Lys Lys Ile Gln Asp Leu Leu
 165 170 175
 Met Ser Phe Gly Ile Leu Lys Pro Asp Leu Arg Ile Val Phe Val His
 180 185 190
 Asn Lys Ala Val Ile Trp Gln Lys Ser Arg Val Ser Asp His Lys Met
 195 200 205
 Ala Leu Met Ser Val Leu Gly Thr Ala Val Met Asn Asn Met Glu Ser
 210 215 220
 Phe Gln Tyr His Ser Glu Glu Ser Gln Ile Tyr Leu Ser Gly Phe Leu
 225 230 235 240
 Pro Lys Cys Asp Ala Asp His Ser Phe Thr Ser Leu Ser Thr Pro Glu
 245 250 255
 Arg Ser Phe Ile Phe Ile Asn Ser Arg Pro Val His Gln Lys Asp Ile
 260 265 270
 Leu Lys Leu Ile Arg His His Tyr Asn Leu Lys Cys Leu Lys Glu Ser
 275 280 285

```

Thr Arg Leu Tyr Pro Val Phe Phe Leu Lys Ile Asp Val Pro Thr Ala
 290                295                300

Asp Val Asp Val Asn Leu Thr Pro Asp Lys Ser Gln Val Leu Leu Gln
305                310                315                320

Asn Lys Glu Ser Val Leu Ile Ala Leu Glu Asn Leu Met Thr Thr Cys
                325                330                335

Tyr Gly Pro Leu Pro Ser Thr Asn Ser Tyr Glu Asn Asn Lys Thr Asp
                340                345                350

Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr Ala Glu Thr Asp Val
                355                360                365

Leu Phe Asn Lys Val Glu Ser Ser Gly Lys Asn Tyr Ser Asn Val Asp
 370                375                380

Thr Ser Val Ile Pro Phe Gln Asn Asp Met His Asn Asp Glu Ser Gly
385                390                395                400

Lys Asn Thr Asp Asp Cys Leu Asn His Gln Ile Ser Ile Gly Asp Phe
                405                410                415

Gly Tyr Gly His Cys Ser Ser Glu Ile Ser Asn Ile Asp Lys Asn Thr
                420                425                430

Lys Asn Ala Phe Gln Asp Ile Ser Met Ser Asn Val Ser Trp Glu Asn
                435                440                445

Ser Gln Thr Glu Tyr Ser Lys Thr Cys Phe Ile Ser Ser Val Lys His
 450                455                460

Thr Gln Ser Glu Asn Gly Asn Lys Asp His Ile Asp Glu Ser Gly Glu
465                470                475                480

Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp
                485                490                495

Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser Val Gly Glu Asn Ile
                500                505                510

Glu Pro Val Lys Ile Leu Val Pro Glu Lys Ser Leu Pro Cys Lys Val
                515                520                525

Ser Asn Asn Asn Tyr Pro Ile Pro Glu Gln Met Asn Leu Asn Glu Asp
 530                535                540

Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn Lys Ser Gly Lys Val
545                550                555                560

```

MOR0251.ST25.txt

Thr Ala Tyr Asp Leu Leu Ser Asn Arg Val Ile Lys Lys Pro Met Ser
 565 570 575

Ala Ser Ala Leu Phe Val Gln Asp His Arg Pro Gln Phe Leu Ile Glu
 580 585 590

Asn Pro Lys Thr Ser Leu Glu Asp Ala Thr Leu Gln Ile Glu Glu Leu
 595 600 605

Trp Lys Thr Leu Ser Glu Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala
 610 615 620

Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met Lys Arg Ala Ile Glu
 625 630 635 640

Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro
 645 650 655

Thr Ser Ala Trp Asn Leu Ala Gln Lys His Lys Leu Lys Thr Ser Leu
 660 665 670

Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln Ser Gln Ile Glu Lys
 675 680 685

Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile Pro Phe Ser Met Lys
 690 695 700

Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys Val Asp Leu Glu Glu
 705 710 715 720

Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg Phe Pro Asp Ala Trp
 725 730 735

Leu Met Thr Ser Lys Thr Glu Val Met Leu Leu Asn Pro Tyr Arg Val
 740 745 750

Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu Asn His Lys Leu Pro
 755 760 765

Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr Glu Ser Leu Phe Asn
 770 775 780

Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met Thr Ala Asp Asp Gln
 785 790 795 800

Arg Tyr Ser Gly Ser Thr Tyr Leu Ser Asp Pro Arg Leu Thr Ala Asn
 805 810 815

Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser Ile Thr Glu Asn Tyr
 820 825 830

Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro Phe Tyr Gly Val Ala
 835 840 845

Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn Arg Asn Ala Lys Glu
850 855 860

Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser Tyr Leu Glu Gly Glu
865 870 875 880

Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr Leu Ser Lys Glu Asp
885 890 895

Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln Phe Gly Asn Glu Ile
900 905 910

Lys Glu Cys Val His Gly Arg Pro Phe Phe His His Leu Thr Tyr Leu
915 920 925

Pro Glu Thr Thr
930

<210> 3
<211> 2771
<212> DNA
<213> Homo sapiens

<400> 3
cgaggcggat cgggtgttgc atccatggag cgagctgaga gctcgagtac agaacctgct 60
aaggccatca aacctattga tcggaagtca gtccatcaga tttgctctgg gcagggtggtta 120
ctgagtctaa gcaactgcgt aaaggagtta gtagaaaaca gtctggatgc tggtgccact 180
aatattgatc taaagcttaa ggactatgga gtggatctta ttgaagtttc agacaatgga 240
tgtggggtag aagaagaaaa cttcgaaggc ttaactctga aacatcacac atctaagatt 300
caagagtttg ccgacctaac tcaggttgaa acttttggct ttcgggggga agctctgagc 360
tcactttgtg cactgagcga tgtcaccatt tctacctgcc acgcatcggc gaaggttgga 420
actcgactga tgtttgatca caatgggaaa attatccaga aaaccccccta cccccgcccc 480
agagggacca cagtcagcgt gcagcagtta ttttccacac tacctgtgcg ccataaggaa 540
tttcaaagga atattaagaa ggagtatgcc aaaatggtcc aggtcttaca tgcatactgt 600
atcatttcag caggcatccg tgtaagttgc accaatcagc ttggacaagg aaaacgacag 660
cctgtggtat gcacaggtgg aagccccagc ataaaggaaa atatcggctc tgtgtttggg 720
cagaagcagt tgcaaagcct cattcctttt gttcagctgc ccctagtga ctccgtgtgt 780
gaagagtacg gtttgagctg ttccgatgct ctgcataatc ttttttacat ctccaggtttc 840
atttcacaat gcacgcatgg agttggaagg agttcaacag acagacagtt tttctttatc 900
aaccggcggc cttgtgacct agcaaaggtc tgcagactcg tgaatgaggt ctaccacatg 960
tataatcgac accagtatcc atttgttggt cttaacattt ctgttgattc agaatgcggt 1020
gatatcaatg ttactccaga taaaaggcaa attttgctac aagaggaaaa gcttttgttg 1080
gcagttttta agacctcttt gataggaatg tttgatagtg atgtcaacaa gctaaatgtc 1140

MOR0251.ST25.txt

```

agtcagcagc cactgctgga tggtgaaggt aacttaataa aaatgcatgc agcggatttg 1200
gaaaagccca tggtagaaaa gcaggatcaa tcccccttcac taaggactgg agaagaaaaa 1260
aaagacgtgt ccatttccag actgcgagag gccttttctc ttcgtcacac aacagagaac 1320
aagcctcaca gcccaaagac tccagaacca agaaggagcc ctctaggaca gaaaaggggt 1380
atgctgtctt ctagcacttc aggtgccatc tctgacaaag gcgtcctgag acctcagaaa 1440
gaggcagtga gttccagtca cggaccaggt gaccctacgg acagagcgga ggtggagaag 1500
gactcggggc acggcagcac ttccgtggat tctgaggggt tcagcatccc agacacgggc 1560
agtcactgca gcagcgagta tgcggccagc tccccagggg acaggggctc gcaggaacat 1620
gtggactctc aggagaaagc gcctgaaact gacgactctt tttcagatgt ggactgccat 1680
tcaaaccagg aagataccgg atgtaaatct cgagttttgc ctcagccaac taatctcgca 1740
accccaaaca caaagcgttt taaaaaagaa gaaattcttt ccagttctga catttgtcaa 1800
aagttagtaa atactcagga catgtcagcc tctcagggtg atgtagctgt gaaaattaat 1860
aagaaagttg tgcccctgga cttttctatg agttctttag ctaaacgaat aaagcagtta 1920
catcatgaag cacagcaaag tgaaggggaa cagaattaca ggaagtttag ggcaaagatt 1980
tgtcctggag aaaatcaagc agccgaagat gaactaagaa aagagataag taaaacgatg 2040
tttgcagaaa tggaaatcat tggtcagttt aacctgggat ttataataac caaactgaat 2100
gaggatatct tcatagtgga ccagcatgcc acggacgaga agtataactt cgagatgctg 2160
cagcagcaca ccgtgctcca ggggcagagg ctcatagcac ctcagactct caacttaact 2220
gctgttaatg aagctgttct gatagaaaat ctggaaatat ttagaaagaa tggctttgat 2280
tttgttatcg atgaaaatgc tccagtcact gaaagggcta aactgatttc cttgccaaact 2340
agtaaaaaact ggaccttcgg accccaggac gtcgatgaac tgatcttcac gctgagcgac 2400
agccctgggg tcatgtgccg gccttcccgga gtcaagcaga tgtttgctc cagagcctgc 2460
cggaagtcgg tgatgattgg gactgctctt aacacaagcg agatgaagaa actgatcacc 2520
cacatggggg agatggacca cccctggaac tgtcccatg gaaggccaac catgagacac 2580
atcgccaacc tgggtgtcat ttctcagaac tgaccgtagt cactgtatgg aataattggt 2640
tttatcgag atttttatgt tttgaaagac agagtcttca ctaacctttt ttgttttaa 2700
atgaaacctg ctacttaaaa aaaatacaca tcacacccat ttaaaagtga tcttgagaac 2760
cttttcaaac c 2771

```

```

<210> 4
<211> 932
<212> PRT
<213> Homo sapiens

```

```
<400> 4
```

```

Met Lys Gln Leu Pro Ala Ala Thr Val Arg Leu Leu Ser Ser Ser Gln
1          5          10          15

```

```

Ile Ile Thr Ser Val Val Ser Val Val Lys Glu Leu Ile Glu Asn Ser
20          25          30

```

Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys Leu Glu Asn Tyr Gly
 35 40 45
 Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val
 50 55 60
 Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser
 65 70 75 80
 His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala
 85 90 95
 Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr
 100 105 110
 Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His
 115 120 125
 Ile Leu Ser Gln Lys Pro Ser His Leu Gly Gln Gly Thr Thr Val Thr
 130 135 140
 Ala Leu Arg Leu Phe Lys Asn Leu Pro Val Arg Lys Gln Phe Tyr Ser
 145 150 155 160
 Thr Ala Lys Lys Cys Lys Asp Glu Ile Lys Lys Ile Gln Asp Leu Leu
 165 170 175
 Met Ser Phe Gly Ile Leu Lys Pro Asp Leu Arg Ile Val Phe Val His
 180 185 190
 Asn Lys Ala Val Ile Trp Gln Lys Ser Arg Val Ser Asp His Lys Met
 195 200 205
 Ala Leu Met Ser Val Leu Gly Thr Ala Val Met Asn Asn Met Glu Ser
 210 215 220
 Phe Gln Tyr His Ser Glu Glu Ser Gln Ile Tyr Leu Ser Gly Phe Leu
 225 230 235 240
 Pro Lys Cys Asp Ala Asp His Ser Phe Thr Ser Leu Ser Thr Pro Glu
 245 250 255
 Arg Ser Phe Ile Phe Ile Asn Ser Arg Pro Val His Gln Lys Asp Ile
 260 265 270
 Leu Lys Leu Ile Arg His His Tyr Asn Leu Lys Cys Leu Lys Glu Ser
 275 280 285
 Thr Arg Leu Tyr Pro Val Phe Phe Leu Lys Ile Asp Val Pro Thr Ala
 290 295 300

MOR0251.ST25.txt

Asp Val Asp Val Asn Leu Thr Pro Asp Lys Ser Gln Val Leu Leu Gln
 305 310 315 320

Asn Lys Glu Ser Val Leu Ile Ala Leu Glu Asn Leu Met Thr Thr Cys
 325 330 335

Tyr Gly Pro Leu Pro Ser Thr Asn Ser Tyr Glu Asn Asn Lys Thr Asp
 340 345 350

Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr Ala Glu Thr Asp Val
 355 360 365

Leu Phe Asn Lys Val Glu Ser Ser Gly Lys Asn Tyr Ser Asn Val Asp
 370 375 380

Thr Ser Val Ile Pro Phe Gln Asn Asp Met His Asn Asp Glu Ser Gly
 385 390 395 400

Lys Asn Thr Asp Asp Cys Leu Asn His Gln Ile Ser Ile Gly Asp Phe
 405 410 415

Gly Tyr Gly His Cys Ser Ser Glu Ile Ser Asn Ile Asp Lys Asn Thr
 420 425 430

Lys Asn Ala Phe Gln Asp Ile Ser Met Ser Asn Val Ser Trp Glu Asn
 435 440 445

Ser Gln Thr Glu Tyr Ser Lys Thr Cys Phe Ile Ser Ser Val Lys His
 450 455 460

Thr Gln Ser Glu Asn Gly Asn Lys Asp His Ile Asp Glu Ser Gly Glu
 465 470 475 480

Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp
 485 490 495

Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser Val Gly Glu Asn Ile
 500 505 510

Glu Pro Val Lys Ile Leu Val Pro Glu Lys Ser Leu Pro Cys Lys Val
 515 520 525

Ser Asn Asn Asn Tyr Pro Ile Pro Glu Gln Met Asn Leu Asn Glu Asp
 530 535 540

Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn Lys Ser Gly Lys Val
 545 550 555 560

Thr Ala Tyr Asp Leu Leu Ser Asn Arg Val Ile Lys Lys Pro Met Ser
 565 570 575

Ala Ser Ala Leu Phe Val Gln Asp His Arg Pro Gln Phe Leu Ile Glu
 580 585 590

Asn Pro Lys Thr Ser Leu Glu Asp Ala Thr Leu Gln Ile Glu Glu Leu
 595 600 605

Trp Lys Thr Leu Ser Glu Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala
 610 615 620

Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met Lys Arg Ala Ile Glu
 625 630 635 640

Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro
 645 650 655

Thr Ser Ala Trp Asn Leu Ala Gln Lys His Lys Leu Lys Thr Ser Leu
 660 665 670

Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln Ser Gln Ile Glu Lys
 675 680 685

Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile Pro Phe Ser Met Lys
 690 695 700

Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys Val Asp Leu Glu Glu
 705 710 715 720

Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg Phe Pro Asp Ala Trp
 725 730 735

Leu Met Thr Ser Lys Thr Glu Val Met Leu Leu Asn Pro Tyr Arg Val
 740 745 750

Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu Asn His Lys Leu Pro
 755 760 765

Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr Glu Ser Leu Phe Asn
 770 775 780

Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met Thr Ala Asp Asp Gln
 785 790 795 800

Arg Tyr Ser Gly Ser Thr Tyr Leu Ser Asp Pro Arg Leu Thr Ala Asn
 805 810 815

Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser Ile Thr Glu Asn Tyr
 820 825 830

Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro Phe Tyr Gly Val Ala
 835 840 845

Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn Arg Asn Ala Lys Glu
 850 855 860

MOR0251.ST25.txt

Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser Tyr Leu Glu Gly Glu
865 870 875 880

Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr Leu Ser Lys Glu Asp
885 890 895

Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln Phe Gly Asn Glu Ile
900 905 910

Lys Glu Cys Val His Gly Arg Pro Phe Phe His His Leu Thr Tyr Leu
915 920 925

Pro Glu Thr Thr
930

<210> 5
<211> 426
<212> DNA
<213> Homo sapiens

<400> 5
cgaggcggat cgggtgttgc atccatggag cgagctgaga gctcgagtac agaacctgct 60
aaggccatca aacctattga tcggaagtca gtccatcaga ttgctctgg gcaggtggta 120
ctgagtctaa gcaactgcggt aaaggagtta gtagaaaaca gtctggatgc tggtgccact 180
aatattgatc taaagcttaa ggactatgga gtggatctta ttgaagtttc agacaatgga 240
tgtggggtag aagaagaaaa cttcgaaggc ttaactctga aacatcacac atctaagatt 300
caagagtttg cgcacctaac tcaggttgaa acttttggct ttcgggggga agctctgagc 360
tcactttgtg cactgagcga tgtcaccatt tctacctgcc acgcatcggc gaaggttgga 420
acttga 426

<210> 6
<211> 133
<212> PRT
<213> Homo sapiens

<400> 6

Met Lys Gln Leu Pro Ala Ala Thr Val Arg Leu Leu Ser Ser Ser Gln
1 5 10 15

Ile Ile Thr Ser Val Val Ser Val Val Lys Glu Leu Ile Glu Asn Ser
20 25 30

Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys Leu Glu Asn Tyr Gly
35 40 45

Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val
50 55 60

Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser
65 70 75 80

His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala
85 90 95

Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr
100 105 110

Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His
115 120 125

Ile Leu Ser Gln Lys
130

<210> 7
<211> 1408
<212> DNA
<213> Homo sapiens

<400> 7
ggcgctccta cctgcaagtg gctagtgcc aagtctgggc cgccgctcct gccgtgcatg 60
ttggggagacc agtacatgca ggtgggctcc acacggagag gggcgagac ccggtgacag 120
ggctttacct ggtacatcgg catggcgcaa ccaagcaag agagggtggc gcgtgccaga 180
caccaacggt cggaaccgc cagacaccaa cggtcggaaa ccgccaagac accaacgctc 240
ggaaaccgcc agacaccaac gctcggaaac cgccagacac caaggctcgg aatccacgcc 300
aggccacgac ggagggcgac tacctccctt ctgacctgc tgctggcggt cggaacaaac 360
gcagtccggt gtgctctgat tgggccaggc tctttgacgt cacggactcg acctttgaca 420
gagccactag gcgaaaagga gagacgggaa gtatTTTTTt cggcccgccc ggaaagggtg 480
gagcacaacg tcgaaagcag ccgttgggag cccaggaggc ggggcgcctg tgggagccgt 540
ggagggaact ttcccagtc ccgaggcgga tccggtgttg catccttgga gcgagctgag 600
aactcga[^]gta cagaacctgc taaggccatc aaacctattg atcgaagtc agtccatcag 660
atttgctctg ggccggtggt accgagtcta aggccgaatg cggatgaagga gttagtagaa 720
aacagtctgg atgctggtgc cactaatgtt gatctaaagc ttaaggacta tggagtggat 780
ctcattgaag ttccaggcaa tggatgtggg gtagaagaag aaaacttcga aggctttact 840
ctgaaacatc acacatgtaa gattcaagag tttgccgacc taactcaggt ggaaactttt 900
ggctttcggg gggaagctct gagctcactt tgtgcactga gtgatgtcac catttctacc 960
tgccgtgtat cagcgaaggt tgggactcga ctggtgtttg atcactatgg gaaaatcatc 1020
cagaaaaccc cctacccccg cccagaggg atgacagtca gcgtgaagca gttatTTTct 1080
acgctacctg tgcaccataa agaatttcaa aggaatatta agaagaaacg tgctgtctc 1140
cccttcgcct tctgccgtga ttgtcagttt cctgaggcct cccagccat gcttcctgta 1200
cagcctgtag aactgactcc tagaagtacc ccacccacc cctgtcctt ggaggacaac 1260
gtgatcactg tattcagctc tgtcaagaat ggtccagggt cttctagatg atctgcacaa 1320
atggttcctc tcctccttcc tgatgtctgc cattagcatt ggaataaagt tcctgctgaa 1380
aatccaaaaa aaaaaaaaaa aaaaaaaa 1408

<210> 8
 <211> 389
 <212> PRT
 <213> Homo sapiens

<400> 8

Met Ala Gln Pro Lys Gln Glu Arg Val Ala Arg Ala Arg His Gln Arg
 1 5 10 15

Ser Glu Thr Ala Arg His Gln Arg Ser Glu Thr Ala Lys Thr Pro Thr
 20 25 30

Leu Gly Asn Arg Gln Thr Pro Thr Leu Gly Asn Arg Gln Thr Pro Arg
 35 40 45

Leu Gly Ile His Ala Arg Pro Arg Arg Arg Ala Thr Thr Ser Leu Leu
 50 55 60

Thr Leu Leu Leu Ala Phe Gly Lys Asn Ala Val Arg Cys Ala Leu Ile
 65 70 75 80

Gly Pro Gly Ser Leu Thr Ser Arg Thr Arg Pro Leu Thr Glu Pro Leu
 85 90 95

Gly Glu Lys Glu Arg Arg Glu Val Phe Phe Pro Pro Arg Pro Glu Arg
 100 105 110

Val Glu His Asn Val Glu Ser Ser Arg Trp Glu Pro Arg Arg Arg Gly
 115 120 125

Ala Cys Gly Ser Arg Gly Gly Asn Phe Pro Ser Pro Arg Gly Gly Ser
 130 135 140

Gly Val Ala Ser Leu Glu Arg Ala Glu Asn Ser Ser Thr Glu Pro Ala
 145 150 155 160

Lys Ala Ile Lys Pro Ile Asp Arg Lys Ser Val His Gln Ile Cys Ser
 165 170 175

Gly Pro Val Val Pro Ser Leu Arg Pro Asn Ala Val Lys Glu Leu Val
 180 185 190

Glu Asn Ser Leu Asp Ala Gly Ala Thr Asn Val Asp Leu Lys Leu Lys
 195 200 205

Asp Tyr Gly Val Asp Leu Ile Glu Val Ser Gly Asn Gly Cys Gly Val
 210 215 220

Glu Glu Glu Asn Phe Glu Gly Phe Thr Leu Lys His His Thr Cys Lys
 225 230 235 240

Ile Gln Glu Phe Ala Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg
 245 250 255

Gly Glu Ala Leu Ser Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser
 260 265 270

Thr Cys Arg Val Ser Ala Lys Val Gly Thr Arg Leu Val Phe Asp His
 275 280 285

Tyr Gly Lys Ile Ile Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Met
 290 295 300

Thr Val Ser Val Lys Gln Leu Phe Ser Thr Leu Pro Val His His Lys
 305 310 315 320

Glu Phe Gln Arg Asn Ile Lys Lys Lys Arg Ala Cys Phe Pro Phe Ala
 325 330 335

Phe Cys Arg Asp Cys Gln Phe Pro Glu Ala Ser Pro Ala Met Leu Pro
 340 345 350

Val Gln Pro Val Glu Leu Thr Pro Arg Ser Thr Pro Pro His Pro Cys
 355 360 365

Ser Leu Glu Asp Asn Val Ile Thr Val Phe Ser Ser Val Lys Asn Gly
 370 375 380

Pro Gly Ser Ser Arg
 385

<210> 9
 <211> 1785
 <212> DNA
 <213> Homo sapiens

<400> 9
 tttttagaaa ctgatgttta ttttccatca accatthtttc catgctgctt aagagaatat 60
 gcaagaacag cttaagacca gtcagtgggt gtcctaccc attcagtggc ctgagcagtg 120
 gggagctgca gaccagtctt ccgtggcagg ctgagcgctc cagtcttcag tagggaattg 180
 ctgaataggc acagagggca cctgtacacc ttcagaccag tctgcaacct caggctgagt 240
 agcagtgaac tcaggagcgg gagcagtgca ttcaccctga aattcctcct tggtcactgc 300
 cttctcagca gcagcctgct cttctttttc aatctcttca ggatctctgt agaagtacag 360
 atcaggcatg acctcccatt ggtgttcacg ggaaatgggt ccacgcatgc gcagaacttc 420
 ccgagccagc atccaccaca ttaaaccac tgagttagct cccttggtgt tgcattggat 480
 ggcaatgtcc acatagcgca gaggagaatc tgtgttacac agcgcaatgg taggtaggtt 540
 aacataagat gcctccgtga gaggcgaagg ggcggcgga cccgggcctg gcccgatatg 600
 gtccttggtg gcctagacta ggccgtcgct gtatgggtgag ccccgaggag gcggatctgg 660
 gccccagaa ggacaccgc ctggatttgc cccgtagccc ggcccgggc cctcgggagc 720
 agaacagcct tggtaggtg gacaggagg gacctcgca gcagacgcgc gcgccagcga 780

MOR0251.ST25.txt

cagcagcccc gccccggcct ctcgggagcc ggggggcaga ggctgcggag cccagagg 840
 gtctatcagc cacagtctct gcatgtttcc aagagcaaca ggaaatgaac acattgcagg 900
 ggccagtgtc attcaaagat gtggctgtgg atttcaccca ggaggagtgg cggcaactgg 960
 accctgatga gaagatagca tacggggatg tgatgttggg gaactacagc catctagttt 1020
 ctgtggggta tgattatcac caagccaaac atcatcatgg agtggagggtg aaggaagtgg 1080
 agcagggaga ggagccgtgg ataatggaag gtgaatttcc atgtcaacat agtccagaac 1140
 ctgctaaggc catcaaacct attgatcgga agtcagtcca tcagatttgc tctgggccag 1200
 tggtagctgag tctaagcact gcagtgaagg agttagtaga aaacagtctg gatgctggtg 1260
 ccactaatat tgatctaaag cttaaggact atggagtggg tctcattgaa gtttcagaca 1320
 atggatgtgg ggtagaagaa gaaaactttg aaggcttaat ctctttcagc tctgaaacat 1380
 cacacatgta agattcaaga gtttgccgac ctaactgaag ttgaaacttt cggttttcag 1440
 ggggaagctc tgagctcact gtgtgcactg agcgatgtca ccattttctac ctgccacgag 1500
 ttggtgaagg ttgggactcg actggtgttt gatcacgatg ggaaaatcat ccaggaaacc 1560
 ccctaccccc accccagagg gaccacagtc agcgtgaagc agttattttc tacgctacct 1620
 gtgcgccata aggaatttca aaggaatatt aagaagacgt gcctgcttcc ctttcgcctt 1680
 ctgccgtgat tgtcagtttc ctgaggcctc cccagccatg cttcctgtac agcctgcaga 1740
 actgtgagtc aattaaacct cttttcttca taaattaaaa aaaaa 1785

<210> 10
 <211> 264
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Cys Pro Trp Arg Pro Arg Leu Gly Arg Arg Cys Met Val Ser Pro
1 5 10 15

Arg Glu Ala Asp Leu Gly Pro Gln Lys Asp Thr Arg Leu Asp Leu Pro
20 25 30

Arg Ser Pro Ala Arg Ala Pro Arg Glu Gln Asn Ser Leu Gly Glu Val
35 40 45

Asp Arg Arg Gly Pro Arg Glu Gln Thr Arg Ala Pro Ala Thr Ala Ala
50 55 60

Pro Pro Arg Pro Leu Gly Ser Arg Gly Ala Glu Ala Ala Glu Pro Gln
65 70 75 80

Glu Gly Leu Ser Ala Thr Val Ser Ala Cys Phe Gln Glu Gln Gln Glu
85 90 95

Met Asn Thr Leu Gln Gly Pro Val Ser Phe Lys Asp Val Ala Val Asp
100 105 110

MOR0251.ST25.txt

Phe Thr Gln Glu Glu Trp Arg Gln Leu Asp Pro Asp Glu Lys Ile Ala
 115 120 125

Tyr Gly Asp Val Met Leu Glu Asn Tyr Ser His Leu Val Ser Val Gly
 130 135 140

Tyr Asp Tyr His Gln Ala Lys His His His Gly Val Glu Val Lys Glu
 145 150 155 160

Val Glu Gln Gly Glu Glu Pro Trp Ile Met Glu Gly Glu Phe Pro Cys
 165 170 175

Gln His Ser Pro Glu Pro Ala Lys Ala Ile Lys Pro Ile Asp Arg Lys
 180 185 190

Ser Val His Gln Ile Cys Ser Gly Pro Val Val Leu Ser Leu Ser Thr
 195 200 205

Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp Ala Gly Ala Thr Asn
 210 215 220

Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp Leu Ile Glu Val Ser
 225 230 235 240

Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe Glu Gly Leu Ile Ser
 245 250 255

Phe Ser Ser Glu Thr Ser His Met
 260

<210> 11
 <211> 2271
 <212> DNA
 <213> Homo sapiens

<400> 11
 atgtcgttcg tggcaggggt tattcggcgg ctggacgaga cagtgggtgaa ccgcatcgcg 60
 gcgggggaag ttatccagcg gccagctaag gctatcaaag agatgattga gaactgttta 120
 gatgcaaaat ccacaagtat tcaagtgatt gttaaagagg gaggcctgaa gttgattcag 180
 atccaagaca atggcaccgg gatcaggaaa gaagatctgg atattgtatg tgaaaggttc 240
 actactagta aactgcagtc ctttgaggat ttagccagta tttctaccta tggctttcga 300
 ggtgaggctt tggccagcat aagccatgtg gctcatgtta ctattacaac gaaaacagct 360
 gatggaaagt gtgcatacag agcaagttac tcagatggaa aactgaaagc ccctcctaaa 420
 ccatgtgctg gcaatcaagg gacccagatc acggtggagg acctttttta caacatagcc 480
 acgaggagaa aagcttttaa aaatccaagt gaagaatatg ggaaaatttt ggaagttggt 540
 ggcaggtatt cagtacacaa tgcaggcatt agtttctcag ttaaaaaaca aggagagaca 600
 gtagctgatg ttaggacact acccaatgcc tcaaccgtgg acaatattcg ctccatcttt 660
 ggaaatgctg ttagtcgaga actgatagaa attggatgtg aggataaaac cctagccttc 720

MOR0251.ST25.txt

```

aaaatgaatg gttacatatc caatgcaaac tactcagtga agaagtgcac cttcttactc 780
ttcatcaacc atcgtctggt agaatcaact tccttgagaa aagccataga aacagtgtat 840
gcagcctatt tgcccaaaaa cacacacca ttctgtacc tcagttaga aatcagtccc 900
cagaatgtgg atgttaatgt gcaccccaca aagcatgaag ttcacttctc gcacgaggag 960
agcatcctgg agcgggtgca gcagcacatc gagagcaagc tcctgggctc caattcctcc 1020
aggatgtact tcaccagac tttgctacca ggacttgctg gccctctgg ggagatggtt 1080
aaatccacaa caagtctgac ctgctcttct acttctggaa gtagtgataa ggtctatgcc 1140
caccagatgg ttctgacaga ttcccggaag cagaagcttg atgcatttct gcagcctctg 1200
agcaaaccctc tgtccagtca gcccaggcc attgtcacag aggataagac agatatttct 1260
agtggcaggg ctaggcagca agatgaggag atgcttgaac tcccagcccc tgctgaagtg 1320
gctgccaaaa atcagagctt ggagggggat acaacaaagg ggacttcaga aatgtcagag 1380
aagagaggac ctacttcag caaccccaga aagagacatc gggaagattc tgatgtggaa 1440
atggtggaag atgattcccg aaaggaaatg actgcagctt gtaccccccg gagaaggatc 1500
attaacctca ctagtgtttt gagtctccag gaagaaatta atgagcaggg acatgaggtt 1560
ctccgggaga tggtgcataa ccaactcttc gtgggctgtg tgaatcctca gtgggccttg 1620
gcacagcatc aaaccaagtt ataccttctc aacaccacca agcttagtga agaactgttc 1680
taccagatac tcatttatga ttttgccaat tttggtgttc tcaggttatc ggagccagca 1740
ccgctctttg accttgccat gcttgcccta gatagtccag agagtggctg gacagaggaa 1800
gatggtccca aagaaggact tgctgaatac attggtgagt ttctgaagaa gaaggctgag 1860
atgcttgcat actatttctc tttggaaatt gatgaggaag ggaacctgat tggattaccc 1920
cttctgattg acaactatgt gcccctttg gagggactgc ctatcttcat tcttcgacta 1980
gccactgagg tgaattggga cgaagaaaag gaatgttttg aaagcctcag taaagaatgc 2040
gctatgttct attccatccg gaagcagtag atatctgagg agtcgacctc ctcaggccag 2100
cagagtgaag tgctggctc cattccaaac tcctggaagt ggactgtgga acacattgtc 2160
tataaagcct tgcgctcaca cattctgcct cctaaacatt tcacagaaga tggaaatata 2220
ctgcagcttg ctaacctgcc tgatctatac aaagtctttg agaggtgtta a 2271

```

<210> 12

<211> 2484

<212> PRT

<213> Homo sapiens

<400> 12

```

Cys Thr Thr Gly Gly Cys Thr Cys Thr Thr Cys Thr Gly Gly Cys Gly
1           5           10           15

```

```

Cys Cys Ala Ala Ala Ala Thr Gly Thr Cys Gly Thr Thr Cys Gly Thr
20           25           30

```

```

Gly Gly Cys Ala Gly Gly Gly Gly Thr Thr Ala Thr Thr Cys Gly Gly
35           40           45

```

Cys Gly Gly Cys Thr Gly Gly Ala Cys Gly Ala Gly Ala Cys Ala Gly
 50 55 60
 Thr Gly Gly Thr Gly Ala Ala Cys Cys Gly Cys Ala Thr Cys Gly Cys
 65 70 75 80
 Gly Gly Cys Gly Gly Gly Gly Gly Ala Ala Gly Thr Thr Ala Thr Cys
 85 90 95
 Cys Ala Gly Cys Gly Gly Cys Cys Ala Gly Cys Thr Ala Ala Thr Gly
 100 105 110
 Cys Thr Ala Thr Cys Ala Ala Ala Gly Ala Gly Ala Thr Gly Ala Thr
 115 120 125
 Thr Gly Ala Gly Ala Ala Cys Thr Gly Thr Thr Thr Ala Gly Ala Thr
 130 135 140
 Gly Cys Ala Ala Ala Ala Thr Cys Cys Ala Cys Ala Ala Gly Thr Ala
 145 150 155 160
 Thr Thr Cys Ala Ala Gly Thr Gly Ala Thr Thr Gly Thr Thr Ala Ala
 165 170 175
 Ala Gly Ala Gly Gly Gly Ala Gly Gly Cys Cys Thr Gly Ala Ala Gly
 180 185 190
 Thr Thr Gly Ala Thr Thr Cys Ala Gly Ala Thr Cys Cys Ala Ala Gly
 195 200 205
 Ala Cys Ala Ala Thr Gly Gly Cys Ala Cys Cys Gly Gly Gly Ala Thr
 210 215 220
 Cys Ala Gly Gly Ala Ala Ala Gly Ala Ala Gly Ala Thr Cys Thr Gly
 225 230 235 240
 Gly Ala Thr Ala Thr Thr Gly Thr Ala Thr Gly Thr Gly Ala Ala Ala
 245 250 255
 Gly Gly Thr Thr Cys Ala Cys Thr Ala Cys Thr Ala Gly Thr Ala Ala
 260 265 270
 Ala Cys Thr Gly Cys Ala Gly Thr Cys Cys Thr Thr Thr Gly Ala Gly
 275 280 285
 Gly Ala Thr Thr Thr Ala Gly Cys Cys Ala Gly Thr Ala Thr Thr Thr
 290 295 300
 Cys Thr Ala Cys Cys Thr Ala Thr Gly Gly Cys Thr Thr Thr Cys Gly
 305 310 315 320

Ala Gly Gly Thr Gly Ala Gly Gly Cys Thr Thr Thr Gly Gly Cys Cys
 325 330 335

Ala Gly Cys Ala Thr Ala Ala Gly Cys Cys Ala Thr Gly Thr Gly Gly
 340 345 350

Cys Thr Cys Ala Thr Gly Thr Thr Ala Cys Thr Ala Thr Thr Ala Cys
 355 360 365

Ala Ala Cys Gly Ala Ala Ala Ala Cys Ala Gly Cys Thr Gly Ala Thr
 370 375 380

Gly Gly Ala Ala Ala Gly Thr Gly Thr Gly Cys Ala Thr Ala Cys Ala
 385 390 395 400

Gly Ala Gly Cys Ala Ala Gly Thr Thr Ala Cys Thr Cys Ala Gly Ala
 405 410 415

Thr Gly Gly Ala Ala Ala Ala Cys Thr Gly Ala Ala Ala Gly Cys Cys
 420 425 430

Cys Cys Thr Cys Cys Thr Ala Ala Ala Cys Cys Ala Thr Gly Thr Gly
 435 440 445

Cys Thr Gly Gly Cys Ala Ala Thr Cys Ala Ala Gly Gly Gly Ala Cys
 450 455 460

Cys Cys Ala Gly Ala Thr Cys Ala Cys Gly Gly Thr Gly Gly Ala Gly
 465 470 475 480

Gly Ala Cys Cys Thr Thr Thr Thr Thr Thr Ala Cys Ala Ala Cys Ala
 485 490 495

Thr Ala Gly Cys Cys Ala Cys Gly Ala Gly Gly Ala Gly Ala Ala Ala
 500 505 510

Ala Gly Cys Thr Thr Thr Ala Ala Ala Ala Ala Thr Cys Cys Ala
 515 520 525

Ala Gly Thr Gly Ala Ala Gly Ala Ala Thr Ala Thr Gly Gly Gly Ala
 530 535 540

Ala Ala Ala Thr Thr Thr Thr Gly Gly Ala Ala Gly Thr Thr Gly Thr
 545 550 555 560

Thr Gly Gly Cys Ala Gly Gly Thr Ala Thr Thr Cys Ala Gly Thr Ala
 565 570 575

Cys Ala Cys Ala Ala Thr Gly Cys Ala Gly Gly Cys Ala Thr Thr Ala
 580 585 590

Gly Thr Thr Thr Cys Thr Cys Ala Gly Thr Thr Ala Ala Ala Ala Ala
 595 600 605

Ala Cys Ala Ala Gly Gly Ala Gly Ala Gly Ala Cys Ala Gly Thr Ala
 610 615 620
 Gly Cys Thr Gly Ala Thr Gly Thr Thr Ala Gly Gly Ala Cys Ala Cys
 625 630 635 640
 Thr Ala Cys Cys Cys Ala Ala Thr Gly Cys Cys Thr Cys Ala Ala Cys
 645 650 655
 Cys Gly Thr Gly Gly Ala Cys Ala Ala Thr Ala Thr Thr Cys Gly Cys
 660 665 670
 Thr Cys Cys Ala Thr Cys Thr Thr Thr Gly Gly Ala Ala Ala Thr Gly
 675 680 685
 Cys Thr Gly Thr Thr Ala Gly Thr Cys Gly Ala Gly Ala Ala Cys Thr
 690 695 700
 Gly Ala Thr Ala Gly Ala Ala Ala Thr Thr Gly Gly Ala Thr Gly Thr
 705 710 715 720
 Gly Ala Gly Gly Ala Thr Ala Ala Ala Ala Cys Cys Cys Thr Ala Gly
 725 730 735
 Cys Cys Thr Thr Cys Ala Ala Ala Ala Thr Gly Ala Ala Thr Gly Gly
 740 745 750
 Thr Thr Ala Cys Ala Thr Ala Thr Cys Cys Ala Ala Thr Gly Cys Ala
 755 760 765
 Ala Ala Cys Thr Ala Cys Thr Cys Ala Gly Thr Gly Ala Ala Gly Ala
 770 775 780
 Ala Gly Thr Gly Cys Ala Thr Cys Thr Thr Cys Thr Thr Ala Cys Thr
 785 790 795 800
 Cys Thr Thr Cys Ala Thr Cys Ala Ala Cys Cys Ala Thr Cys Gly Thr
 805 810 815
 Cys Thr Gly Gly Thr Ala Gly Ala Ala Thr Cys Ala Ala Cys Thr Thr
 820 825 830
 Cys Cys Thr Thr Gly Ala Gly Ala Ala Ala Ala Gly Cys Cys Ala Thr
 835 840 845
 Ala Gly Ala Ala Ala Cys Ala Gly Thr Gly Thr Ala Thr Gly Cys Ala
 850 855 860
 Gly Cys Cys Thr Ala Thr Thr Thr Gly Cys Cys Cys Ala Ala Ala Ala
 865 870 875 880

Ala Cys Ala Cys Ala Cys Ala Cys Cys Cys Ala Thr Thr Cys Cys Thr
885 890 895

Gly Thr Ala Cys Cys Thr Cys Ala Gly Thr Thr Thr Ala Gly Ala Ala
900 905 910

Ala Thr Cys Ala Gly Thr Cys Cys Cys Cys Ala Gly Ala Ala Thr Gly
915 920 925

Thr Gly Gly Ala Thr Gly Thr Thr Ala Ala Thr Gly Thr Gly Cys Ala
930 935 940

Cys Cys Cys Cys Ala Cys Ala Ala Ala Gly Cys Ala Thr Gly Ala Ala
945 950 955 960

Gly Thr Thr Cys Ala Cys Thr Thr Cys Cys Thr Gly Cys Ala Cys Gly
965 970 975

Ala Gly Gly Ala Gly Ala Gly Cys Ala Thr Cys Cys Thr Gly Gly Ala
980 985 990

Gly Cys Gly Gly Gly Thr Gly Cys Ala Gly Cys Ala Gly Cys Ala Cys
995 1000 1005

Ala Thr Cys Gly Ala Gly Ala Gly Cys Ala Ala Gly Cys Thr Cys
1010 1015 1020

Cys Thr Gly Gly Gly Cys Thr Cys Cys Ala Ala Thr Thr Cys Cys
1025 1030 1035

Thr Cys Cys Ala Gly Gly Ala Thr Gly Thr Ala Cys Thr Thr Cys
1040 1045 1050

Ala Cys Cys Cys Ala Gly Ala Cys Thr Thr Thr Gly Cys Thr Ala
1055 1060 1065

Cys Cys Ala Gly Gly Ala Cys Thr Thr Gly Cys Thr Gly Gly Cys
1070 1075 1080

Cys Cys Cys Thr Cys Thr Gly Gly Gly Gly Ala Gly Ala Thr Gly
1085 1090 1095

Gly Thr Thr Ala Ala Ala Thr Cys Cys Ala Cys Ala Ala Cys Ala
1100 1105 1110

Ala Gly Thr Cys Thr Gly Ala Cys Cys Thr Cys Gly Thr Cys Thr
1115 1120 1125

Thr Cys Thr Ala Cys Thr Thr Cys Thr Gly Gly Ala Ala Gly Thr
1130 1135 1140

Ala Gly Thr Gly Ala Thr Ala Ala Gly Gly Thr Cys Thr Ala Thr
1145 1150 1155

Gly Cys Cys Cys Ala Cys Cys Ala Gly Ala Thr Gly Gly Thr Thr
 1160 1165 1170
 Cys Gly Thr Ala Cys Ala Gly Ala Thr Thr Cys Cys Cys Gly Gly
 1175 1180 1185
 Gly Ala Ala Cys Ala Gly Ala Ala Gly Cys Thr Thr Gly Ala Thr
 1190 1195 1200
 Gly Cys Ala Thr Thr Thr Cys Thr Gly Cys Ala Gly Cys Cys Thr
 1205 1210 1215
 Cys Thr Gly Ala Gly Cys Ala Ala Ala Cys Cys Cys Cys Thr Gly
 1220 1225 1230
 Thr Cys Cys Ala Gly Thr Cys Ala Gly Cys Cys Cys Cys Ala Gly
 1235 1240 1245
 Gly Cys Cys Ala Thr Thr Gly Thr Cys Ala Cys Ala Gly Ala Gly
 1250 1255 1260
 Gly Ala Thr Ala Ala Gly Ala Cys Ala Gly Ala Thr Ala Thr Thr
 1265 1270 1275
 Thr Cys Thr Ala Gly Thr Gly Gly Cys Ala Gly Gly Gly Cys Thr
 1280 1285 1290
 Ala Gly Gly Cys Ala Gly Cys Ala Ala Gly Ala Thr Gly Ala Gly
 1295 1300 1305
 Gly Ala Gly Ala Thr Gly Cys Thr Thr Gly Ala Ala Cys Thr Cys
 1310 1315 1320
 Cys Cys Ala Gly Cys Cys Cys Cys Thr Gly Cys Thr Gly Ala Ala
 1325 1330 1335
 Gly Thr Gly Gly Cys Thr Gly Cys Cys Ala Ala Ala Ala Ala Thr
 1340 1345 1350
 Cys Ala Gly Ala Gly Cys Thr Thr Gly Gly Ala Gly Gly Gly Gly
 1355 1360 1365
 Gly Ala Thr Ala Cys Ala Ala Cys Ala Ala Ala Gly Gly Gly Gly
 1370 1375 1380
 Ala Cys Thr Thr Cys Ala Gly Ala Ala Ala Thr Gly Thr Cys Ala
 1385 1390 1395
 Gly Ala Gly Ala Ala Gly Ala Gly Ala Gly Gly Ala Cys Cys Thr
 1400 1405 1410

Ala Cys Thr Thr Cys Cys Ala Gly Cys Ala Ala Cys Cys Cys Cys	1415	1420	1425
Ala Gly Ala Ala Ala Gly Ala Gly Ala Cys Ala Thr Cys Gly Gly	1430	1435	1440
Gly Ala Ala Gly Ala Thr Thr Cys Thr Gly Ala Thr Gly Thr Gly	1445	1450	1455
Gly Ala Ala Ala Thr Gly Gly Thr Gly Gly Ala Ala Gly Ala Thr	1460	1465	1470
Gly Ala Thr Thr Cys Cys Cys Gly Ala Ala Ala Gly Gly Ala Ala	1475	1480	1485
Ala Thr Gly Ala Cys Thr Gly Cys Ala Gly Cys Thr Thr Gly Thr	1490	1495	1500
Ala Cys Cys Cys Cys Cys Gly Gly Ala Gly Ala Ala Gly Gly	1505	1510	1515
Ala Thr Cys Ala Thr Thr Ala Ala Cys Cys Thr Cys Ala Cys Thr	1520	1525	1530
Ala Gly Thr Gly Thr Thr Thr Thr Gly Ala Gly Thr Cys Thr Cys	1535	1540	1545
Cys Ala Gly Gly Ala Ala Gly Ala Ala Ala Thr Thr Ala Ala Thr	1550	1555	1560
Gly Ala Gly Cys Ala Gly Gly Gly Ala Cys Ala Thr Gly Ala Gly	1565	1570	1575
Gly Thr Thr Cys Thr Cys Cys Gly Gly Gly Ala Gly Ala Thr Gly	1580	1585	1590
Thr Thr Gly Cys Ala Thr Ala Ala Cys Cys Ala Cys Thr Cys Cys	1595	1600	1605
Thr Thr Cys Gly Thr Gly Gly Gly Cys Thr Gly Thr Gly Thr Gly	1610	1615	1620
Ala Ala Thr Cys Cys Thr Cys Ala Gly Thr Gly Gly Gly Cys Cys	1625	1630	1635
Thr Thr Gly Gly Cys Ala Cys Ala Gly Cys Ala Thr Cys Ala Ala	1640	1645	1650
Ala Cys Cys Ala Ala Gly Thr Thr Ala Thr Ala Cys Cys Thr Thr	1655	1660	1665
Cys Thr Cys Ala Ala Cys Ala Cys Cys Ala Cys Cys Ala Ala Gly	1670	1675	1680

Cys Thr Thr Ala Gly Thr Gly Ala Ala Gly Ala Ala Cys Thr Gly
 1685 1690 1695
 Thr Thr Cys Thr Ala Cys Cys Ala Gly Ala Thr Ala Cys Thr Cys
 1700 1705 1710
 Ala Thr Thr Thr Ala Thr Gly Ala Thr Thr Thr Thr Gly Cys Cys
 1715 1720 1725
 Ala Ala Thr Thr Thr Thr Gly Gly Thr Gly Thr Thr Cys Thr Cys
 1730 1735 1740
 Ala Gly Gly Thr Thr Ala Thr Cys Gly Gly Ala Gly Cys Cys Ala
 1745 1750 1755
 Gly Cys Ala Cys Cys Gly Cys Thr Cys Thr Thr Thr Gly Ala Cys
 1760 1765 1770
 Cys Thr Thr Gly Cys Cys Ala Thr Gly Cys Thr Thr Gly Cys Cys
 1775 1780 1785
 Thr Thr Ala Gly Ala Thr Ala Gly Thr Cys Cys Ala Gly Ala Gly
 1790 1795 1800
 Ala Gly Thr Gly Gly Cys Thr Gly Gly Ala Cys Ala Gly Ala Gly
 1805 1810 1815
 Gly Ala Ala Gly Ala Thr Gly Gly Thr Cys Cys Cys Ala Ala Ala
 1820 1825 1830
 Gly Ala Ala Gly Gly Ala Cys Thr Thr Gly Cys Thr Gly Ala Ala
 1835 1840 1845
 Thr Ala Cys Ala Thr Thr Gly Thr Thr Gly Ala Gly Thr Thr Thr
 1850 1855 1860
 Cys Thr Gly Ala Ala Gly Ala Ala Gly Ala Ala Gly Gly Cys Thr
 1865 1870 1875
 Gly Ala Gly Ala Thr Gly Cys Thr Thr Gly Cys Ala Gly Ala Cys
 1880 1885 1890
 Thr Ala Thr Thr Thr Cys Thr Cys Thr Thr Thr Gly Gly Ala Ala
 1895 1900 1905
 Ala Thr Thr Gly Ala Thr Gly Ala Gly Gly Ala Ala Gly Gly Gly
 1910 1915 1920
 Ala Ala Cys Cys Thr Gly Ala Thr Thr Gly Gly Ala Thr Thr Ala
 1925 1930 1935

Cys 1940	Cys	Cys	Thr	Thr	Cys 1945	Thr	Gly	Ala	Thr	Thr	Gly	Ala	Cys	1950
Ala 1955	Ala	Cys	Thr	Ala	Thr	Gly 1960	Thr	Gly	Cys	Cys	Cys	Cys	Cys	Thr
Thr 1970	Thr	Gly	Gly	Ala	Gly	Gly 1975	Gly	Ala	Cys	Thr	Gly 1980	Cys	Cys	Thr
Ala 1985	Thr	Cys	Thr	Thr	Cys	Ala 1990	Thr	Thr	Cys	Thr	Thr 1995	Cys	Gly	Ala
Cys 2000	Thr	Ala	Gly	Cys	Cys	Ala 2005	Cys	Thr	Gly	Ala	Gly 2010	Gly	Thr	Gly
Ala 2015	Ala	Thr	Thr	Gly	Gly	Gly 2020	Ala	Cys	Gly	Ala	Ala 2025	Gly	Ala	Ala
Ala 2030	Ala	Gly	Gly	Ala	Ala	Thr 2035	Gly	Thr	Thr	Thr	Thr 2040	Gly	Ala	Ala
Ala 2045	Gly	Cys	Cys	Thr	Cys	Ala 2050	Gly	Thr	Ala	Ala	Ala 2055	Gly	Ala	Ala
Thr 2060	Gly	Cys	Gly	Cys	Thr	Ala 2065	Thr	Gly	Thr	Thr	Cys 2070	Thr	Ala	Thr
Thr 2075	Cys	Cys	Ala	Thr	Cys	Cys 2080	Gly	Gly	Ala	Ala	Gly 2085	Cys	Ala	Gly
Thr 2090	Ala	Cys	Ala	Thr	Ala	Thr 2095	Cys	Thr	Gly	Ala	Gly 2100	Gly	Ala	Gly
Thr 2105	Cys	Gly	Ala	Cys	Cys	Cys 2110	Thr	Cys	Thr	Cys	Ala 2115	Gly	Gly	Cys
Cys 2120	Ala	Gly	Cys	Ala	Gly	Ala 2125	Gly	Thr	Gly	Ala	Ala 2130	Gly	Thr	Gly
Cys 2135	Cys	Thr	Gly	Gly	Cys	Thr 2140	Cys	Cys	Ala	Thr	Thr 2145	Cys	Cys	Ala
Ala 2150	Ala	Cys	Thr	Cys	Cys	Thr 2155	Gly	Gly	Ala	Ala	Gly 2160	Thr	Gly	Gly
Ala 2165	Cys	Thr	Gly	Thr	Gly	Gly 2170	Ala	Ala	Cys	Ala	Cys 2175	Ala	Thr	Thr
Gly 2180	Thr	Cys	Thr	Ala	Thr	Ala 2185	Ala	Ala	Gly	Cys	Cys 2190	Thr	Thr	Gly
Cys 2195	Gly	Cys	Thr	Cys	Ala	Cys 2200	Ala	Cys	Ala	Thr	Thr 2205	Cys	Thr	Gly

Cys Cys Thr Cys Cys Thr Ala Ala Ala Cys Ala Thr Thr Thr Cys
 2210 2215 2220
 Ala Cys Ala Gly Ala Ala Gly Ala Thr Gly Gly Ala Ala Ala Thr
 2225 2230 2235
 Ala Thr Cys Cys Thr Gly Cys Ala Gly Cys Thr Thr Gly Cys Thr
 2240 2245 2250
 Ala Ala Cys Cys Thr Gly Cys Cys Thr Gly Ala Thr Cys Thr Ala
 2255 2260 2265
 Thr Ala Cys Ala Ala Ala Gly Thr Cys Thr Thr Thr Gly Ala Gly
 2270 2275 2280
 Ala Gly Gly Thr Gly Thr Thr Ala Ala Ala Thr Ala Thr Gly Gly
 2285 2290 2295
 Thr Thr Ala Thr Thr Thr Ala Thr Gly Cys Ala Cys Thr Gly Thr
 2300 2305 2310
 Gly Gly Gly Ala Thr Gly Thr Gly Thr Thr Cys Thr Thr Cys Thr
 2315 2320 2325
 Thr Thr Cys Thr Cys Thr Gly Thr Ala Thr Thr Cys Cys Gly Ala
 2330 2335 2340
 Thr Ala Cys Ala Ala Ala Gly Thr Gly Thr Thr Gly Thr Ala Thr
 2345 2350 2355
 Cys Ala Ala Ala Gly Thr Gly Thr Gly Ala Thr Ala Thr Ala Cys
 2360 2365 2370
 Ala Ala Ala Gly Thr Gly Thr Ala Cys Cys Ala Ala Cys Ala Thr
 2375 2380 2385
 Ala Ala Gly Thr Gly Thr Thr Gly Gly Thr Ala Gly Cys Ala Cys
 2390 2395 2400
 Thr Thr Ala Ala Gly Ala Cys Thr Thr Ala Thr Ala Cys Thr Thr
 2405 2410 2415
 Gly Cys Cys Thr Thr Cys Thr Gly Ala Thr Ala Gly Thr Ala Thr
 2420 2425 2430
 Thr Cys Cys Thr Thr Thr Ala Thr Ala Cys Ala Cys Ala Gly Thr
 2435 2440 2445
 Gly Gly Ala Thr Thr Gly Ala Thr Thr Ala Thr Ala Ala Ala Thr
 2450 2455 2460

Ala Ala Ala Thr Ala Gly Ala Thr Gly Thr Gly Thr Cys Thr Thr
 2465 2470 2475

Ala Ala Cys Ala Thr Ala
 2480

<210> 13
 <211> 4895
 <212> DNA
 <213> Homo sapiens

<400> 13
 gtcggcgctcc gaggcggttg gtgtcggaga atttgtaag cgggactcca ggcaattatt 60
 tccagtcaga gaaggaaacc agtgcctggc attctcacca tctttctacc taccatgac 120
 aagtgtctgt cagttgaagt acaagccaaa ttgcgttctg gtttggccat aagctccttg 180
 ggccaatgtg ttgaggaact tgccctcaac agtattgatg ctgaagcaaa atgtgtggct 240
 gtcagggtga atatggaaac cttccaagtt caagtgatag acaatggatt tgggatgggg 300
 agtgatgatg tagagaaagt gggaaatcgt tatttcacca gtaaatgcca ctcggtacag 360
 gacttggaga atccaagggtt ttatggtttc cgaggagagg ccttggcaaa tattgctgac 420
 atggccagtg ctgtggaaat ttcgtccaag aaaaacagga caatgaaaac ttttgtgaaa 480
 ctgtttcaga gtggaaaagc cctgaaagct tgtgaagctg atgtgactag agcaagcgct 540
 gggactactg taacagtgtg taacctatct taccagcttc ctgtaaggag gaaatgcatg 600
 gaccctagac tggagtttga gaaggttagg cagagaatag aagctctctc actcatgcac 660
 ccttccatctt ctttctcttt gagaaatgat gtttctgggtt ccatggttct tcagctccct 720
 aaaaccaaag acgtatgttc ccgattttgt caaatttatg gattgggaaa gtcccaaaag 780
 ctaagagaaa taagttttta atataaagag tttgagctta gtggctatat cagctctgaa 840
 gcacattaca acaagaatat gcagtttttg tttgtgaaca aaagactagt ttaaggaca 900
 aagctacata aactcattga ctttttatta aggaaagaaa gtattatatg caagccaaag 960
 aatggtccca ccagtaggca aatgaattca agtcttcggc accggtctac ccagaaactc 1020
 tatggcatat atgtaattaa tgtgcagtgc caattctgtg agtatgatgt gtgcatggag 1080
 ccagccaaaa ctctgattga atttcagaac tgggacactc tcttgtttg cattcaggaa 1140
 ggagtgaaaa tgtttttaaa gcaagaaaaa ttatttgtgg aattatcagg tgaggatatt 1200
 aaggaattta gtgaagataa tggtttttagt ttatttgatg ctactcttca gaagcgtgtg 1260
 acttccgatg agaggagcaa tttccaggaa gcatgtaata atattttaga ttcctatgag 1320
 atgtttaatt tgcagtcaaa agctgtgaaa agaaaaacta ctgcagaaaa cgtaaacaca 1380
 cagagtctta gggattcaga agctaccaga aaaaatacaa atgatgcatt tttgtacatt 1440
 tatgaatcag gtggtccagg ccatagcaaa atgacagagc catctttaca aaacaaagac 1500
 agctcttgct cagaatcaaa gatgttagaa caagagacaa ttgtagcatc agaagctggt 1560
 gaaaatgaga aacataaaaa atctttcctg gaacgtagct ctttagaaaa tccgtgtgga 1620
 accagtttag aaatgttttt aagccctttt cagacaccat gtcactttga ggagagtggg 1680

MOR0251.ST25.txt

caggatctag	aaatatggaa	agaaagtact	actgttaatg	gcatggctgc	caacatcttg	1740
aaaaataata	gaattcagaa	tcaaccaaag	agattttaaag	atgctactga	agtgggatgc	1800
cagcctctgc	cttttgcaac	aacattatgg	ggagtacata	gtgctcagac	agagaaagag	1860
aaaaaaaaaag	aatctagcaa	ttgtggaaga	agaaatgttt	ttagttatgg	gcgagttaaa	1920
ttatgttcca	ctggctttat	aactcatgta	gtacaaaatg	aaaaaactaa	atcaactgaa	1980
acagaacatt	catttaaaaa	ttatgttaga	cctgggtccca	cacgtgccca	agaaacattt	2040
ggaaatagaa	cacgtcattc	agttgaaact	ccagacatca	aagatttagc	cagcacttta	2100
agtaaagaat	ctgggtcaatt	gccaacaaaa	aaaaattgca	gaacgaatat	aagttatggg	2160
ctagagaatg	aacctacagc	aacttataca	atgttttctg	cttttcagga	aggtagcaaa	2220
aatcacaaa	cagattgcat	attatctgat	acatccccct	ctttccccctg	gtatagacac	2280
gtttccaatg	atagtaggaa	aacagataaa	ttaattgggt	tctccaaacc	aatcgtccgt	2340
aagaagctaa	gcttgagttc	acagctagga	tcttttagaga	agtttaagag	gcaatatggg	2400
aaggttgaaa	atcctctgga	tacagaagta	gaggaaagta	atggagtcac	taccaatctc	2460
agtcttcaag	ttgaacctga	cattctgctg	aaggacaaga	accgcttaga	gaactctgat	2520
gtttgtaaaa	tactactat	ggagcatagt	gattcagata	gtagttgtca	accagcaagc	2580
cacatccttg	actcagagaa	gtttccattc	tccaaggatg	aagattgttt	agaacaacag	2640
atgcctagtt	tgagagaaa	tcctatgacc	ctgaaggagt	tatctctctt	taatagaaaa	2700
cctttggacc	ttgagaagtc	atctgaatca	ctagcctcta	aattatccag	actgaagggt	2760
tccgaaagag	aaactcaaac	aatggggatg	atgagtcgtt	ttaatgaact	tccaaattca	2820
gattccagta	ggaaagacag	caagttgtgc	agtgtgttaa	cacaagattt	ttgtatgtta	2880
tttaacaaca	agcatgaaaa	aacagagaat	ggtgtcatcc	caacatcaga	ttctgccaca	2940
caggataatt	cctttaataa	aaatagtaaa	acacattcta	acagcaatac	aacagagAAC	3000
tgtgtgatat	cagaaactcc	tttggtattg	ccctataata	attctaaagt	taccggtaaa	3060
gattcagatg	ttcttatcag	agcctcagaa	caacagatag	gaagtcttga	ctctcccagt	3120
ggaatgttaa	tgaatccggt	agaagatgcc	acaggtgacc	aaaatggaat	ttgttttcag	3180
agtgaggaat	ctaaagcaag	agcttgttct	gaaactgaag	agtcaaacac	gtgttgttca	3240
gattggcagc	ggcatttcga	tgtagccctg	ggaagaatgg	tttatgtcaa	caaaatgact	3300
ggactcagca	cattcattgc	cccaactgag	gacattcagg	ctgcttgtag	taaagacctg	3360
acaactgtgg	ctgtggatgt	tgtacttgag	aatgggtctc	agtacagggtg	tcaacctttt	3420
agaagcgacc	ttgttcttcc	tttccttccg	agagctcgag	cagagaggac	tgtgatgaga	3480
caggataaca	gagatactgt	ggatgatact	gttagtagcg	aatcgcttca	gtctttgttc	3540
tcagaatggg	acaatccagt	atttgcccgt	tatccagagg	ttgctgttga	tgtaagcagt	3600
ggccaggctg	agagcttagc	agttaaaatt	cacaacatct	tgtatcccta	tcgtttcacc	3660
aaaggaatga	ttcattcaat	gcaggttctc	cagcaagtag	ataacaagtt	tattgcctgt	3720
ttgatgagca	ctaagactga	agagaatggc	gaggcagatt	cctacgagaa	gcaacaggca	3780

MOR0251.ST25.txt

```

caaggctctg gtcggaaaaa attactgtct tctactctaa ttcctccgct agagataaca 3840
gtgacagagg aacaaaggag actcttatgg tgttaccaca aaaatctgga agatctgggc 3900
cttgaatttg tatttccaga cactagtgat tctctgggcc ttgtgggaaa agtaccacta 3960
tgttttgtgg aaagagaagc caatgaactt cggagaggaa gatctactgt gaccaagagt 4020
attgtggagg aatttatccg agaacaactg gagctactcc agaccaccgg aggcattcaa 4080
gggacattgc cactgactgt ccagaagggt ttggcatccc aagcctgcc tggggccatt 4140
aagtttaatg atggcctgag cttacaggaa agttgccgcc ttattgaagc tctgtcctca 4200
tgccagctgc cattccagtg tgctcacggg agaccttcta tgctgccgtt agctgacata 4260
gaccacttgg aacaggaaaa acagattaaa cccaacctca ctaaacttcg caaaatggcc 4320
caggcctggc gtctcttttg aaaagcagag tgtgatacaa ggcagagcct gcagcagtcc 4380
atgcctccct gtgagccacc atgagaacag aatcactggg ctaaaaggaa caaagggatg 4440
ttcactgtat gcctctgagc agagagcagc agcagcaggt accagcacgg ccctgactga 4500
atcagcccag tgcctctgag cagcttagac agcagggctc tctgtatcag tctttcttga 4560
gcagatgatt cccctagttg agtagccaga tgaaattcaa gcctaaagac aattcattca 4620
tttgcatcca tgggcacaga aggttgctat atagtatcta ctttttgcta cttatttaat 4680
gataaaattht aatgacagtt taaaaaaaaa aaaaaaaaaa attatttgaa ggggtgggtg 4740
atthttgttht ttgtacagtt ttttttcaag cttcacattht gcgtgtatct aattcagctg 4800
atgctcaagt ccaaggggta gtctgccttc ccaggctgcc cccagggtht ctgactgggt 4860
ccctctthtt cccttcagtc ttcttcactt ccctt 4895

```

```

<210> 14
<211> 1429
<212> PRT
<213> Homo sapiens

```

```
<400> 14
```

```
Met Ile Lys Cys Leu Ser Val Glu Val Gln Ala Lys Leu Arg Ser Gly
1          5          10          15
```

```
Leu Ala Ile Ser Ser Leu Gly Gln Cys Val Glu Glu Leu Ala Leu Asn
20          25          30
```

```
Ser Ile Asp Ala Glu Ala Lys Cys Val Ala Val Arg Val Asn Met Glu
35          40          45
```

```
Thr Phe Gln Val Gln Val Ile Asp Asn Gly Phe Gly Met Gly Ser Asp
50          55          60
```

```
Asp Val Glu Lys Val Gly Asn Arg Tyr Phe Thr Ser Lys Cys His Ser
65          70          75          80
```

```
Val Gln Asp Leu Glu Asn Pro Arg Phe Tyr Gly Phe Arg Gly Glu Ala
85          90          95
```

MOR0251.ST25.txt

Leu Ala Asn Ile Ala Asp Met Ala Ser Ala Val Glu Ile Ser Ser Lys
 100 105 110

Lys Asn Arg Thr Met Lys Thr Phe Val Lys Leu Phe Gln Ser Gly Lys
 115 120 125

Ala Leu Lys Ala Cys Glu Ala Asp Val Thr Arg Ala Ser Ala Gly Thr
 130 135 140

Thr Val Thr Val Tyr Asn Leu Phe Tyr Gln Leu Pro Val Arg Arg Lys
 145 150 155 160

Cys Met Asp Pro Arg Leu Glu Phe Glu Lys Val Arg Gln Arg Ile Glu
 165 170 175

Ala Leu Ser Leu Met His Pro Ser Ile Ser Phe Ser Leu Arg Asn Asp
 180 185 190

Val Ser Gly Ser Met Val Leu Gln Leu Pro Lys Thr Lys Asp Val Cys
 195 200 205

Ser Arg Phe Cys Gln Ile Tyr Gly Leu Gly Lys Ser Gln Lys Leu Arg
 210 215 220

Glu Ile Ser Phe Lys Tyr Lys Glu Phe Glu Leu Ser Gly Tyr Ile Ser
 225 230 235 240

Ser Glu Ala His Tyr Asn Lys Asn Met Gln Phe Leu Phe Val Asn Lys
 245 250 255

Arg Leu Val Leu Arg Thr Lys Leu His Lys Leu Ile Asp Phe Leu Leu
 260 265 270

Arg Lys Glu Ser Ile Ile Cys Lys Pro Lys Asn Gly Pro Thr Ser Arg
 275 280 285

Gln Met Asn Ser Ser Leu Arg His Arg Ser Thr Pro Glu Leu Tyr Gly
 290 295 300

Ile Tyr Val Ile Asn Val Gln Cys Gln Phe Cys Glu Tyr Asp Val Cys
 305 310 315 320

Met Glu Pro Ala Lys Thr Leu Ile Glu Phe Gln Asn Trp Asp Thr Leu
 325 330 335

Leu Phe Cys Ile Gln Glu Gly Val Lys Met Phe Leu Lys Gln Glu Lys
 340 345 350

Leu Phe Val Glu Leu Ser Gly Glu Asp Ile Lys Glu Phe Ser Glu Asp
 355 360 365

Asn Gly Phe Ser Leu Phe Asp Ala Thr Leu Gln Lys Arg Val Thr Ser
 370 375 380

Asp Glu Arg Ser Asn Phe Gln Glu Ala Cys Asn Asn Ile Leu Asp Ser
 385 390 395 400
 Tyr Glu Met Phe Asn Leu Gln Ser Lys Ala Val Lys Arg Lys Thr Thr
 405 410 415
 Ala Glu Asn Val Asn Thr Gln Ser Ser Arg Asp Ser Glu Ala Thr Arg
 420 425 430
 Lys Asn Thr Asn Asp Ala Phe Leu Tyr Ile Tyr Glu Ser Gly Gly Pro
 435 440 445
 Gly His Ser Lys Met Thr Glu Pro Ser Leu Gln Asn Lys Asp Ser Ser
 450 455 460
 Cys Ser Glu Ser Lys Met Leu Glu Gln Glu Thr Ile Val Ala Ser Glu
 465 470 475 480
 Ala Gly Glu Asn Glu Lys His Lys Lys Ser Phe Leu Glu Arg Ser Ser
 485 490 495
 Leu Glu Asn Pro Cys Gly Thr Ser Leu Glu Met Phe Leu Ser Pro Phe
 500 505 510
 Gln Thr Pro Cys His Phe Glu Glu Ser Gly Gln Asp Leu Glu Ile Trp
 515 520 525
 Lys Glu Ser Thr Thr Val Asn Gly Met Ala Ala Asn Ile Leu Lys Asn
 530 535 540
 Asn Arg Ile Gln Asn Gln Pro Lys Arg Phe Lys Asp Ala Thr Glu Val
 545 550 555 560
 Gly Cys Gln Pro Leu Pro Phe Ala Thr Thr Leu Trp Gly Val His Ser
 565 570 575
 Ala Gln Thr Glu Lys Glu Lys Lys Lys Glu Ser Ser Asn Cys Gly Arg
 580 585 590
 Arg Asn Val Phe Ser Tyr Gly Arg Val Lys Leu Cys Ser Thr Gly Phe
 595 600 605
 Ile Thr His Val Val Gln Asn Glu Lys Thr Lys Ser Thr Glu Thr Glu
 610 615 620
 His Ser Phe Lys Asn Tyr Val Arg Pro Gly Pro Thr Arg Ala Gln Glu
 625 630 635 640
 Thr Phe Gly Asn Arg Thr Arg His Ser Val Glu Thr Pro Asp Ile Lys
 645 650 655

MOR0251.ST25.txt

Asp Leu Ala Ser Thr Leu Ser Lys Glu Ser Gly Gln Leu Pro Asn Lys
 660 665 670

Lys Asn Cys Arg Thr Asn Ile Ser Tyr Gly Leu Glu Asn Glu Pro Thr
 675 680 685

Ala Thr Tyr Thr Met Phe Ser Ala Phe Gln Glu Gly Ser Lys Lys Ser
 690 695 700

Gln Thr Asp Cys Ile Leu Ser Asp Thr Ser Pro Ser Phe Pro Trp Tyr
 705 710 715 720

Arg His Val Ser Asn Asp Ser Arg Lys Thr Asp Lys Leu Ile Gly Phe
 725 730 735

Ser Lys Pro Ile Val Arg Lys Lys Leu Ser Leu Ser Ser Gln Leu Gly
 740 745 750

Ser Leu Glu Lys Phe Lys Arg Gln Tyr Gly Lys Val Glu Asn Pro Leu
 755 760 765

Asp Thr Glu Val Glu Glu Ser Asn Gly Val Thr Thr Asn Leu Ser Leu
 770 775 780

Gln Val Glu Pro Asp Ile Leu Leu Lys Asp Lys Asn Arg Leu Glu Asn
 785 790 795 800

Ser Asp Val Cys Lys Ile Thr Thr Met Glu His Ser Asp Ser Asp Ser
 805 810 815

Ser Cys Gln Pro Ala Ser His Ile Leu Asp Ser Glu Lys Phe Pro Phe
 820 825 830

Ser Lys Asp Glu Asp Cys Leu Glu Gln Gln Met Pro Ser Leu Arg Glu
 835 840 845

Ser Pro Met Thr Leu Lys Glu Leu Ser Leu Phe Asn Arg Lys Pro Leu
 850 855 860

Asp Leu Glu Lys Ser Ser Glu Ser Leu Ala Ser Lys Leu Ser Arg Leu
 865 870 875 880

Lys Gly Ser Glu Arg Glu Thr Gln Thr Met Gly Met Met Ser Arg Phe
 885 890 895

Asn Glu Leu Pro Asn Ser Asp Ser Ser Arg Lys Asp Ser Lys Leu Cys
 900 905 910

Ser Val Leu Thr Gln Asp Phe Cys Met Leu Phe Asn Asn Lys His Glu
 915 920 925

Lys Thr Glu Asn Gly Val Ile Pro Thr Ser Asp Ser Ala Thr Gln Asp
 930 935 940


```

Asn Ser Phe Asn Lys Asn Ser Lys Thr His Ser Asn Ser Asn Thr Thr
945                      950                      955                      960

Glu Asn Cys Val Ile Ser Glu Thr Pro Leu Val Leu Pro Tyr Asn Asn
                      965                      970                      975

Ser Lys Val Thr Gly Lys Asp Ser Asp Val Leu Ile Arg Ala Ser Glu
                      980                      985                      990

Gln Gln Ile Gly Ser Leu Asp Ser Pro Ser Gly Met Leu Met Asn Pro
                      995                      1000                      1005

Val Glu Asp Ala Thr Gly Asp Gln Asn Gly Ile Cys Phe Gln Ser
1010                      1015                      1020

Glu Glu Ser Lys Ala Arg Ala Cys Ser Glu Thr Glu Glu Ser Asn
1025                      1030                      1035

Thr Cys Cys Ser Asp Trp Gln Arg His Phe Asp Val Ala Leu Gly
1040                      1045                      1050

Arg Met Val Tyr Val Asn Lys Met Thr Gly Leu Ser Thr Phe Ile
1055                      1060                      1065

Ala Pro Thr Glu Asp Ile Gln Ala Ala Cys Thr Lys Asp Leu Thr
1070                      1075                      1080

Thr Val Ala Val Asp Val Val Leu Glu Asn Gly Ser Gln Tyr Arg
1085                      1090                      1095

Cys Gln Pro Phe Arg Ser Asp Leu Val Leu Pro Phe Leu Pro Arg
1100                      1105                      1110

Ala Arg Ala Glu Arg Thr Val Met Arg Gln Asp Asn Arg Asp Thr
1115                      1120                      1125

Val Asp Asp Thr Val Ser Ser Glu Ser Leu Gln Ser Leu Phe Ser
1130                      1135                      1140

Glu Trp Asp Asn Pro Val Phe Ala Arg Tyr Pro Glu Val Ala Val
1145                      1150                      1155

Asp Val Ser Ser Gly Gln Ala Glu Ser Leu Ala Val Lys Ile His
1160                      1165                      1170

Asn Ile Leu Tyr Pro Tyr Arg Phe Thr Lys Gly Met Ile His Ser
1175                      1180                      1185

Met Gln Val Leu Gln Gln Val Asp Asn Lys Phe Ile Ala Cys Leu
1190                      1195                      1200

```

Met Ser Thr Lys Thr Glu Glu Asn Gly Glu Ala Asp Ser Tyr Glu
1205 1210 1215

Lys Gln Gln Ala Gln Gly Ser Gly Arg Lys Lys Leu Leu Ser Ser
1220 1225 1230

Thr Leu Ile Pro Pro Leu Glu Ile Thr Val Thr Glu Glu Gln Arg
1235 1240 1245

Arg Leu Leu Trp Cys Tyr His Lys Asn Leu Glu Asp Leu Gly Leu
1250 1255 1260

Glu Phe Val Phe Pro Asp Thr Ser Asp Ser Leu Val Leu Val Gly
1265 1270 1275

Lys Val Pro Leu Cys Phe Val Glu Arg Glu Ala Asn Glu Leu Arg
1280 1285 1290

Arg Gly Arg Ser Thr Val Thr Lys Ser Ile Val Glu Glu Phe Ile
1295 1300 1305

Arg Glu Gln Leu Glu Leu Leu Gln Thr Thr Gly Gly Ile Gln Gly
1310 1315 1320

Thr Leu Pro Leu Thr Val Gln Lys Val Leu Ala Ser Gln Ala Cys
1325 1330 1335

His Gly Ala Ile Lys Phe Asn Asp Gly Leu Ser Leu Gln Glu Ser
1340 1345 1350

Cys Arg Leu Ile Glu Ala Leu Ser Ser Cys Gln Leu Pro Phe Gln
1355 1360 1365

Cys Ala His Gly Arg Pro Ser Met Leu Pro Leu Ala Asp Ile Asp
1370 1375 1380

His Leu Glu Gln Glu Lys Gln Ile Lys Pro Asn Leu Thr Lys Leu
1385 1390 1395

Arg Lys Met Ala Gln Ala Trp Arg Leu Phe Gly Lys Ala Glu Cys
1400 1405 1410

Asp Thr Arg Gln Ser Leu Gln Gln Ser Met Pro Pro Cys Glu Pro
1415 1420 1425

Pro

<210> 15
<211> 3145
<212> DNA
<213> Homo sapiens

<400> 15

MOR0251.ST25.txt

ggcgggaaac agcttagtggt gtgtgggggtc gcgcatttttc ttcaaccagg aggtgaggag	60
gtttcgacat ggcggtgcag ccgaaggaga cgctgcagtt ggagagcgcg gccgaggtcg	120
gcttcgtgcy cttcttttcag ggcatgccgg agaagccgac caccacagtg cgccttttcg	180
accggggcga cttctatacg gcgcacggcg aggcgcgcgt gctggccgcc cgggagggtgt	240
tcaagacca gggggtgatc aagtacatgg ggccggcagg agcaaagaat ctgcagagtgt	300
ttgtgcttag taaaatgaat tttgaatctt ttgtaaaaga tcttcttctg gttcgtcagt	360
atagagttga agtttataag aatagagctg gaaataaggc atccaaggag aatgattggt	420
atgtggcata taaggcttct cctggcaatc tctctcagtt tgaagacatt ctcttttgta	480
acaatgatat gtcagcttcc attggtgttg tgggtgttaa aatgtccgca gttgatggcc	540
agagacaggt tggagttggg tatgtggatt ccatacagag gaaactagga ctgtgtgaat	600
tccctgataa tgatcagttc tccaatcttg aggcctctct catccagatt ggaccaaaagg	660
aatgtgtttt acccgaggga gagactgctg gagacatggg gaaactgaga cagataattc	720
aaagaggagg aattctgatc acagaaagaa aaaaagctga cttttccaca aaagacattt	780
atcaggacct caaccggttg ttgaaaggca aaaagggaga gcagatgaat agtgcgttat	840
tgccagaaat ggagaatcag gttgcagttt catcactgtc tgcggtaatc aagttttttag	900
aactcttata agatgattcc aactttggac agtttgaact gactactttt gacttcagcc	960
agtatatgaa attggatatt gcagcagtc gagcccttaa cttttttcag ggttctgttg	1020
aagataccac tggctctcag tctctggctg ctttgctgaa taagtgtaaa acccctcaag	1080
gacaaagact tgttaaccag tggattaagc agcctctcat ggataagaac agaatagagg	1140
agagattgaa tttagtggaa gctttttag aagatgcaga attgaggcag actttacaag	1200
aagatttact tcgtcgattc ccagatctta accgacttgc caagaagttt caaagacaag	1260
cagcaaaactt acaagattgt taccgactct atcagggtat aaatcaacta cctaattgta	1320
tacaggctct ggaaaaacat gaaggaaaac accagaaatt attggttgga gtttttgtga	1380
ctcctcttac tgatcttcgt tctgacttct ccaagtttca ggaaatgata gaaacaactt	1440
tagatatgga tcaggtggaa aaccatgaat tccttgtaaa accttcattt gatcctaate	1500
tcagtgaatt aagagaaata atgaatgact tggaaaagaa gatgcagtc acattaataa	1560
gtgcagccag agatcttggc ttggaccctg gcaaacagat taaactggat tccagtgcac	1620
agtttgata ttactttcgt gtaacctgta aggaagaaaa agtccttcgt aacaataaaa	1680
acttttagtac tgtagatata cagaagaatg gtgttaaatt taccaacagc aaattgactt	1740
ctttaaatga agagtatacc aaaaataaaa cagaatatga agaagcccag gatgccattg	1800
ttaaagaaat tgtcaatatt tcttcaggct atgtagaacc aatgcagaca ctcaatgatg	1860
tgtagctca gctagatgct gttgtcagct ttgctcacgt gtcaaatgga gcacctgttc	1920
catatgtacg accagccatt ttggagaaag gacaaggaag aattatatta aaagcatcca	1980
ggcatgcttg tgttgaagtt caagatgaaa ttgcatttat tcctaataac gtatactttg	2040
aaaaagataa acagatgttc cacatcatta ctggcccaa tatgggagggt aaatcaacat	2100

MOR0251.ST25.txt

atattcgaca aactggggtg atagtactca tggcccaaat tgggtgtttt gtgccatgtg 2160
 agtcagcaga agtgtccatt gtggactgca tcttagcccg agtaggggct ggtgacagtc 2220
 aattgaaagg agtctccacg ttcattggctg aaatgttgga aactgcttct atcctcaggt 2280
 ctgcaaccaa agattcatta ataatcatag atgaattggg aagaggaact tctacctacg 2340
 atggatttgg gttagcatgg gctatatcag aatacattgc aacaaagatt ggtgcttttt 2400
 gcatgtttgc aacccatttt catgaactta ctgccttggc caatcagata ccaactgtta 2460
 ataatctaca tgtcacagca ctcaccactg aagagacctt aactatgctt tatcaggtga 2520
 agaaagggtg ctgtgatcaa agttttggga ttcattgttg agagcttgct aatttcccta 2580
 agcatgtaat agagtgtgct aaacagaaaag ccctggaact tgaggagttt cagtatatgt 2640
 gagaatcgca aggatatgat atcatggaac cagcagcaaa gaagtgcctat ctggaaagag 2700
 agcaagggtg aaaaattatt caggagttcc tgtccaaggt gaaacaaatg ccctttactg 2760
 aaatgtcaga agaaaacatc acaataaagt taaaacagct aaaagctgaa gtaatagcaa 2820
 agaataatag ctttgtaa at gaaatcattt cacgaataaa agttactacg tgaaaaatcc 2880
 cagtaatgga atgaaggtaa tattgataag ctattgtctg taatagtttt atattgtttt 2940
 atattaaccc tttttccata gtgttaactg tcagtgccca tgggctatca acttaataag 3000
 atatttagta atattttact ttgaggacat tttcaaagat ttttattttg aaaaatgaga 3060
 gctgtaactg aggactgttt gcaattgaca taggcaataa taagtgatgt gctgaatttt 3120
 ataaataaaa tcatgtagtt tgtgg 3145

<210> 16
 <211> 934
 <212> PRT
 <213> Homo sapiens

<400> 16

Met Ala Val Gln Pro Lys Glu Thr Leu Gln Leu Glu Ser Ala Ala Glu
1 5 10 15

Val Gly Phe Val Arg Phe Phe Gln Gly Met Pro Glu Lys Pro Thr Thr
20 25 30

Thr Val Arg Leu Phe Asp Arg Gly Asp Phe Tyr Thr Ala His Gly Glu
35 40 45

Asp Ala Leu Leu Ala Ala Arg Glu Val Phe Lys Thr Gln Gly Val Ile
50 55 60

Lys Tyr Met Gly Pro Ala Gly Ala Lys Asn Leu Gln Ser Val Val Leu
65 70 75 80

Ser Lys Met Asn Phe Glu Ser Phe Val Lys Asp Leu Leu Leu Val Arg
85 90 95

Gln Tyr Arg Val Glu Val Tyr Lys Asn Arg Ala Gly Asn Lys Ala Ser
100 105 110

Lys Glu Asn Asp Trp Tyr Leu Ala Tyr Lys Ala Ser Pro Gly Asn Leu
 115 120 125
 Ser Gln Phe Glu Asp Ile Leu Phe Gly Asn Asn Asp Met Ser Ala Ser
 130 135 140
 Ile Gly Val Val Gly Val Lys Met Ser Ala Val Asp Gly Gln Arg Gln
 145 150 155 160
 Val Gly Val Gly Tyr Val Asp Ser Ile Gln Arg Lys Leu Gly Leu Cys
 165 170 175
 Glu Phe Pro Asp Asn Asp Gln Phe Ser Asn Leu Glu Ala Leu Leu Ile
 180 185 190
 Gln Ile Gly Pro Lys Glu Cys Val Leu Pro Gly Gly Glu Thr Ala Gly
 195 200 205
 Asp Met Gly Lys Leu Arg Gln Ile Ile Gln Arg Gly Gly Ile Leu Ile
 210 215 220
 Thr Glu Arg Lys Lys Ala Asp Phe Ser Thr Lys Asp Ile Tyr Gln Asp
 225 230 235 240
 Leu Asn Arg Leu Leu Lys Gly Lys Lys Gly Glu Gln Met Asn Ser Ala
 245 250 255
 Val Leu Pro Glu Met Glu Asn Gln Val Ala Val Ser Ser Leu Ser Ala
 260 265 270
 Val Ile Lys Phe Leu Glu Leu Leu Ser Asp Asp Ser Asn Phe Gly Gln
 275 280 285
 Phe Glu Leu Thr Thr Phe Asp Phe Ser Gln Tyr Met Lys Leu Asp Ile
 290 295 300
 Ala Ala Val Arg Ala Leu Asn Leu Phe Gln Gly Ser Val Glu Asp Thr
 305 310 315 320
 Thr Gly Ser Gln Ser Leu Ala Ala Leu Leu Asn Lys Cys Lys Thr Pro
 325 330 335
 Gln Gly Gln Arg Leu Val Asn Gln Trp Ile Lys Gln Pro Leu Met Asp
 340 345 350
 Lys Asn Arg Ile Glu Glu Arg Leu Asn Leu Val Glu Ala Phe Val Glu
 355 360 365
 Asp Ala Glu Leu Arg Gln Thr Leu Gln Glu Asp Leu Leu Arg Arg Phe
 370 375 380

MOR0251.ST25.txt

Pro Asp Leu Asn Arg Leu Ala Lys Lys Phe Gln Arg Gln Ala Ala Asn
 385 390 395 400

Leu Gln Asp Cys Tyr Arg Leu Tyr Gln Gly Ile Asn Gln Leu Pro Asn
 405 410 415

Val Ile Gln Ala Leu Glu Lys His Glu Gly Lys His Gln Lys Leu Leu
 420 425 430

Leu Ala Val Phe Val Thr Pro Leu Thr Asp Leu Arg Ser Asp Phe Ser
 435 440 445

Lys Phe Gln Glu Met Ile Glu Thr Thr Leu Asp Met Asp Gln Val Glu
 450 455 460

Asn His Glu Phe Leu Val Lys Pro Ser Phe Asp Pro Asn Leu Ser Glu
 465 470 475 480

Leu Arg Glu Ile Met Asn Asp Leu Glu Lys Lys Met Gln Ser Thr Leu
 485 490 495

Ile Ser Ala Ala Arg Asp Leu Gly Leu Asp Pro Gly Lys Gln Ile Lys
 500 505 510

Leu Asp Ser Ser Ala Gln Phe Gly Tyr Tyr Phe Arg Val Thr Cys Lys
 515 520 525

Glu Glu Lys Val Leu Arg Asn Asn Lys Asn Phe Ser Thr Val Asp Ile
 530 535 540

Gln Lys Asn Gly Val Lys Phe Thr Asn Ser Lys Leu Thr Ser Leu Asn
 545 550 555 560

Glu Glu Tyr Thr Lys Asn Lys Thr Glu Tyr Glu Glu Ala Gln Asp Ala
 565 570 575

Ile Val Lys Glu Ile Val Asn Ile Ser Ser Gly Tyr Val Glu Pro Met
 580 585 590

Gln Thr Leu Asn Asp Val Leu Ala Gln Leu Asp Ala Val Val Ser Phe
 595 600 605

Ala His Val Ser Asn Gly Ala Pro Val Pro Tyr Val Arg Pro Ala Ile
 610 615 620

Leu Glu Lys Gly Gln Gly Arg Ile Ile Leu Lys Ala Ser Arg His Ala
 625 630 635 640

Cys Val Glu Val Gln Asp Glu Ile Ala Phe Ile Pro Asn Asp Val Tyr
 645 650 655

Phe Glu Lys Asp Lys Gln Met Phe His Ile Ile Thr Gly Pro Asn Met
 660 665 670

Gly Gly Lys Ser Thr Tyr Ile Arg Gln Thr Gly Val Ile Val Leu Met
 675 680 685
 Ala Gln Ile Gly Cys Phe Val Pro Cys Glu Ser Ala Glu Val Ser Ile
 690 695 700
 Val Asp Cys Ile Leu Ala Arg Val Gly Ala Gly Asp Ser Gln Leu Lys
 705 710 715 720
 Gly Val Ser Thr Phe Met Ala Glu Met Leu Glu Thr Ala Ser Ile Leu
 725 730 735
 Arg Ser Ala Thr Lys Asp Ser Leu Ile Ile Ile Asp Glu Leu Gly Arg
 740 745 750
 Gly Thr Ser Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Ser Glu
 755 760 765
 Tyr Ile Ala Thr Lys Ile Gly Ala Phe Cys Met Phe Ala Thr His Phe
 770 775 780
 His Glu Leu Thr Ala Leu Ala Asn Gln Ile Pro Thr Val Asn Asn Leu
 785 790 795 800
 His Val Thr Ala Leu Thr Thr Glu Glu Thr Leu Thr Met Leu Tyr Gln
 805 810 815
 Val Lys Lys Gly Val Cys Asp Gln Ser Phe Gly Ile His Val Ala Glu
 820 825 830
 Leu Ala Asn Phe Pro Lys His Val Ile Glu Cys Ala Lys Gln Lys Ala
 835 840 845
 Leu Glu Leu Glu Glu Phe Gln Tyr Ile Gly Glu Ser Gln Gly Tyr Asp
 850 855 860
 Ile Met Glu Pro Ala Ala Lys Lys Cys Tyr Leu Glu Arg Glu Gln Gly
 865 870 875 880
 Glu Lys Ile Ile Gln Glu Phe Leu Ser Lys Val Lys Gln Met Pro Phe
 885 890 895
 Thr Glu Met Ser Glu Glu Asn Ile Thr Ile Lys Leu Lys Gln Leu Lys
 900 905 910
 Ala Glu Val Ile Ala Lys Asn Asn Ser Phe Val Asn Glu Ile Ile Ser
 915 920 925
 Arg Ile Lys Val Thr Thr
 930

<210> 17
 <211> 4374
 <212> DNA
 <213> Homo sapiens

<400> 17
 gggcacgagc cctgccatgt ctgcgccgaa gcctgcgtcg ggcggcctcg ctgcctccag 60
 ctcagcccct gcgaggcaag cggttttgag ccgattcttc cagtctacgg gaagcctgaa 120
 atccacctcc tctccacag gtgcagccga ccaggtggac cctggcgctg cagcggccgc 180
 agcgccccca ggcggcgct tcccgcccc gctgccgccc cacgtagcta cagaaattga 240
 cagaagaaag aagagaccat tggaaaatga tgggcctgtt aaaaagaaag taaagaaagt 300
 ccaacaaaag gaaggaggaa gtgatctggg aatgtctggc aactctgagc caaagaaatg 360
 tctgaggacc aggaatgttt caaagtctct gaaaaaattg aaagaattct gctgcgattc 420
 tgcccttcct caaagtagag tccagacaga atctctgcag gagagatttg cagttctgcc 480
 aaaatgtact gattttgatg atatcagtct tctacacgca aagaatgcag tttcttctga 540
 agattcgaaa cgtcaaatta atcaaaagga cacaacactt tttgatctca gtcagtttgg 600
 atcatcaa atcaagtcag aaaatttaca gaaaactgct tccaaatcag ctaacaaacg 660
 gtccaaaagc atctatacgc cgctagaatt acaatacata gaaatgaagc agcagcacia 720
 agatgcagtt ttgtgtgtgg aatgtggata taagtataga ttctttgggg aagatgcaga 780
 gattgcagcc cgagagctca atattttattg ccatttagat cacaacttta tgacagcaag 840
 tatactact cacagactgt ttgttcatgt acgccgcctg gtggcaaaag gatataaggt 900
 gggagtgtg aagcaaaactg aaactgcagc attaaaggcc attggagaca acagaagtgc 960
 actcttttcc cggaattga ctgcccttta tacaaaatct acacttattg gagaagatgt 1020
 gaatccccta atcaagctgg atgatgctgt aaatgttgat gagataatga ctgatacttc 1080
 taccagctat cttctgtgca tctctgaaaa taaggaaaat gttagggaca aaaaaaaggg 1140
 caacattttt attggcattg tgggagtgcg gcctgccaca ggcgagggtg tgtttgatag 1200
 tttccaggac tctgcttctc gttcagagct agaaacccgg atgtcaagcc tgcagccagt 1260
 agagctgctg cttccttcgg ccttgtccga gcaaacagag gcgctcatcc acagagccac 1320
 atctgttagt gtgcaggatg acagaattcg agtcgaaagg atggataaca tttattttga 1380
 atacagccat gctttccagg cagttacaga gttttatgca aaagatacag ttgacatcaa 1440
 aggtttctcaa attatttctg gcattgttaa cttagagaag cctgtgattt gctctttggc 1500
 tgccatcata aaatacctca aagaattcaa cttggaaaag atgctctcca aacctgagaa 1560
 ttttaaacag ctatcaagta aaatggaatt tatgacaatt aatggaacaa cattaaggaa 1620
 tctggaaatc ctacagaatc agactgatat gaaaaccaa ggaagtgtgc tgtgggtttt 1680
 agaccacact aaaacttcat ttgggagacg gaagttaaag aagtgggtga cccagccact 1740
 ccttaaatta agggaaataa atgcccggct tgatgctgta tcggaagtgc tccattcaga 1800
 atctagtgtg tttggtcaga tagaaaatca tctacgtaaa ttgcccagca tagagagggg 1860
 actctgtagc atttatcaca aaaaatgttc tacccaagag ttcttcttga ttgtcaaaac 1920

MOR0251.ST25.txt

tttatatcac	ctaaagtcag	aatttcaagc	aataatacct	gctgttaatt	cccacattca	1980
gtcagacttg	ctccggaccg	ttatttttaga	aattcctgaa	ctcctcagtc	cagtggagca	2040
ttacttaaaag	atactcaatg	aacaagctgc	caaagttggg	gataaaactg	aattatttaa	2100
agacctttct	gacttccctt	taataaaaaa	gaggaaggat	gaaattcaag	gtgttattga	2160
cgagatccga	atgcatttgc	aagaaatacg	aaaaatacta	aaaaatcctt	ctgcacaata	2220
tgtgacagta	tcaggacagg	agtttatgat	agaaataaag	aactctgctg	tatcttgtat	2280
accaactgat	tgggtaaagg	ttggaagcac	aaaagctgtg	agccgctttc	actctccttt	2340
tattgtagaa	aattacagac	atctgaatca	gctccgggag	cagctagtc	ttgactgcag	2400
tgctgaatgg	cttgattttc	tagagaaatt	cagtgaacat	tatcactcct	tgtgtaaagg	2460
agtgcacac	ctagcaactg	ttgactgcat	tttctccctg	gccaaagtcg	ctaagcaagg	2520
agattactgc	agaccaactg	tacaagaaga	aagaaaaatt	gtaataaaaa	atggaaggca	2580
ccctgtgatt	gatgtgttgc	tgggagaaca	ggatcaatat	gtcccaaata	atacagattt	2640
atcagaggac	tcagagagag	taatgataat	taccggacca	aacatgggtg	gaaagagctc	2700
ctacataaaa	caagttgcat	tgattaccat	catggctcag	attggctcct	atgttcctgc	2760
agaagaagcg	acaattggga	ttgtggatgg	cattttcaca	aggatgggtg	ctgcagacaa	2820
tatatataaa	ggacggagta	catttatgga	agaactgact	gacacagcag	aaataatcag	2880
aaaagcaaca	tcacagtcct	tggttatcct	ggatgaacta	ggaagaggga	cgagcactca	2940
tgatggaatt	gccattgcct	atgctacact	tgagtatttc	atcagagatg	tgaaatcctt	3000
aaccctgttt	gtcaccatt	atccgccagt	ttgtgaacta	gaaaaaaatt	actcacacca	3060
ggtggggaat	taccacatgg	gattcttggg	cagtgaggat	gaaagcaaac	tggatccagg	3120
cgcagcagaa	caagtccttg	attttgtcac	cttcctttac	caaataacta	gaggaattgc	3180
agcaaggagt	tatggattaa	atgtggctaa	actagcagat	gttcctggag	aaattttgaa	3240
gaaagcagct	cacaagtcaa	aagagctgga	aggattaata	aatacgaaaa	gaaagagact	3300
caagtatttt	gcaaagttat	ggacgatgca	taatgcacaa	gacctgcaga	agtggacaga	3360
ggagtccaac	atggaagaaa	cacagacttc	tcttcttcac	taaaatgaag	actacatttg	3420
tgaacaaaaa	atggagaatt	aaaaatacca	actgtacaaa	ataactctcc	agtaacagcc	3480
tatctttgtg	tgacatgtga	gcataaaatt	atgaccatgg	tatatctcta	ttggaaacag	3540
agagggtttt	ctgaagacag	tctttttcaa	gtttctgtct	tcctaacttt	tctacgtata	3600
aacactcttg	aatagacttc	cactttgtaa	ttagaaaatt	ttatggacag	taagtccagt	3660
aaagccttaa	gtggcagaat	ataattccca	agcttttgga	gggtgatata	aaaatttact	3720
tgatatTTTT	atTTgtttca	gttcagataa	ttggcaactg	ggtgaatctg	gcaggaatct	3780
atccattgaa	ctaaaataat	tttattatgc	aaçcagttta	tccaccaaga	acataagaat	3840
tttttataag	tagaaagaat	tggccaggca	tgggtggctca	tgcttgaat	cccagcactt	3900
tgggaggcca	aggtaggcag	atcacctgag	gtcaggagtt	caagaccagc	ctggccaaca	3960
tggcaaaacc	ccatctttac	taaaaatata	aagtacatct	ctactaaaaa	tacgaaaaaa	4020

MOR0251.ST25.txt

ttagctgggc atggtggcgc acacctgtag tcccagctac tccggaggct gaggcaggag 4080
 aatctcttga acctgggagg cggaggttgc aatgagccga gatcacgtca ctgcactcca 4140
 gcttgggcaa cagagcaaga ctccatctca aaaaagaaaa aagaaaagaa atagaattat 4200
 caagctttta aaaactagag cacagaagga ataaggtcat gaaatttaaa aggttaaata 4260
 ttgtcatagg attaagcagt ttaaagattg ttggatgaaa ttatttgtca ttcattcaag 4320
 taataaatat ttaatgaata cttgctataa aaaaaaaaaa aaaaaaaaaa aaaa 4374

<210> 18
 <211> 1128
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Ser Arg Arg Lys Pro Ala Ser Gly Gly Leu Ala Ala Ser Ser Ser
1 5 10 15

Ala Pro Ala Arg Gln Ala Val Leu Ser Arg Phe Phe Gln Ser Thr Gly
20 25 30

Ser Leu Lys Ser Thr Ser Ser Ser Thr Gly Ala Ala Asp Gln Val Asp
35 40 45

Pro Gly Ala Ala Ala Ala Ala Ala Pro Pro Ala Pro Ala Phe Pro Pro
50 55 60

Gln Leu Pro Pro His Val Ala Thr Glu Ile Asp Arg Arg Lys Lys Arg
65 70 75 80

Pro Leu Glu Asn Asp Gly Pro Val Lys Lys Lys Val Lys Lys Val Gln
85 90 95

Gln Lys Glu Gly Gly Ser Asp Leu Gly Met Ser Gly Asn Ser Glu Pro
100 105 110

Lys Lys Cys Leu Arg Thr Arg Asn Val Ser Lys Ser Leu Glu Lys Leu
115 120 125

Lys Glu Phe Cys Cys Asp Ser Ala Leu Pro Gln Ser Arg Val Gln Thr
130 135 140

Glu Ser Leu Gln Glu Arg Phe Ala Val Leu Pro Lys Cys Thr Asp Phe
145 150 155 160

Asp Asp Ile Ser Leu Leu His Ala Lys Asn Ala Val Ser Ser Glu Asp
165 170 175

Ser Lys Arg Gln Ile Asn Gln Lys Asp Thr Thr Leu Phe Asp Leu Ser
180 185 190

Gln Phe Gly Ser Ser Asn Thr Ser His Glu Asn Leu Gln Lys Thr Ala
195 200 205

Ser Lys Ser Ala Asn Lys Arg Ser Lys Ser Ile Tyr Thr Pro Leu Glu
 210 215 220
 Leu Gln Tyr Ile Glu Met Lys Gln Gln His Lys Asp Ala Val Leu Cys
 225 230 235 240
 Val Glu Cys Gly Tyr Lys Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile
 245 250 255
 Ala Ala Arg Glu Leu Asn Ile Tyr Cys His Leu Asp His Asn Phe Met
 260 265 270
 Thr Ala Ser Ile Pro Thr His Arg Leu Phe Val His Val Arg Arg Leu
 275 280 285
 Val Ala Lys Gly Tyr Lys Val Gly Val Val Lys Gln Thr Glu Thr Ala
 290 295 300
 Ala Leu Lys Ala Ile Gly Asp Asn Arg Ser Ser Leu Phe Ser Arg Lys
 305 310 315 320
 Leu Thr Ala Leu Tyr Thr Lys Ser Thr Leu Ile Gly Glu Asp Val Asn
 325 330 335
 Pro Leu Ile Lys Leu Asp Asp Ala Val Asn Val Asp Glu Ile Met Thr
 340 345 350
 Asp Thr Ser Thr Ser Tyr Leu Leu Cys Ile Ser Glu Asn Lys Glu Asn
 355 360 365
 Val Arg Asp Lys Lys Lys Gly Asn Ile Phe Ile Gly Ile Val Gly Val
 370 375 380
 Gln Pro Ala Thr Gly Glu Val Val Phe Asp Ser Phe Gln Asp Ser Ala
 385 390 395 400
 Ser Arg Ser Glu Leu Glu Thr Arg Met Ser Ser Leu Gln Pro Val Glu
 405 410 415
 Leu Leu Leu Pro Ser Ala Leu Ser Glu Gln Thr Glu Ala Leu Ile His
 420 425 430
 Arg Ala Thr Ser Val Ser Val Gln Asp Asp Arg Ile Arg Val Glu Arg
 435 440 445
 Met Asp Asn Ile Tyr Phe Glu Tyr Ser His Ala Phe Gln Ala Val Thr
 450 455 460
 Glu Phe Tyr Ala Lys Asp Thr Val Asp Ile Lys Gly Ser Gln Ile Ile
 465 470 475 480

MOR0251.ST25.txt

Ser Gly Ile Val Asn Leu Glu Lys Pro Val Ile Cys Ser Leu Ala Ala
 485 490 495

Ile Ile Lys Tyr Leu Lys Glu Phe Asn Leu Glu Lys Met Leu Ser Lys
 500 505 510

Pro Glu Asn Phe Lys Gln Leu Ser Ser Lys Met Glu Phe Met Thr Ile
 515 520 525

Asn Gly Thr Thr Leu Arg Asn Leu Glu Ile Leu Gln Asn Gln Thr Asp
 530 535 540

Met Lys Thr Lys Gly Ser Leu Leu Trp Val Leu Asp His Thr Lys Thr
 545 550 555 560

Ser Phe Gly Arg Arg Lys Leu Lys Lys Trp Val Thr Gln Pro Leu Leu
 565 570 575

Lys Leu Arg Glu Ile Asn Ala Arg Leu Asp Ala Val Ser Glu Val Leu
 580 585 590

His Ser Glu Ser Ser Val Phe Gly Gln Ile Glu Asn His Leu Arg Lys
 595 600 605

Leu Pro Asp Ile Glu Arg Gly Leu Cys Ser Ile Tyr His Lys Lys Cys
 610 615 620

Ser Thr Gln Glu Phe Phe Leu Ile Val Lys Thr Leu Tyr His Leu Lys
 625 630 635 640

Ser Glu Phe Gln Ala Ile Ile Pro Ala Val Asn Ser His Ile Gln Ser
 645 650 655

Asp Leu Leu Arg Thr Val Ile Leu Glu Ile Pro Glu Leu Leu Ser Pro
 660 665 670

Val Glu His Tyr Leu Lys Ile Leu Asn Glu Gln Ala Ala Lys Val Gly
 675 680 685

Asp Lys Thr Glu Leu Phe Lys Asp Leu Ser Asp Phe Pro Leu Ile Lys
 690 695 700

Lys Arg Lys Asp Glu Ile Gln Gly Val Ile Asp Glu Ile Arg Met His
 705 710 715 720

Leu Gln Glu Ile Arg Lys Ile Leu Lys Asn Pro Ser Ala Gln Tyr Val
 725 730 735

Thr Val Ser Gly Gln Glu Phe Met Ile Glu Ile Lys Asn Ser Ala Val
 740 745 750

Ser Cys Ile Pro Thr Asp Trp Val Lys Val Gly Ser Thr Lys Ala Val
 755 760 765

Ser Arg Phe His Ser Pro Phe Ile Val Glu Asn Tyr Arg His Leu Asn
 770 775 780

Gln Leu Arg Glu Gln Leu Val Leu Asp Cys Ser Ala Glu Trp Leu Asp
 785 790 795 800

Phe Leu Glu Lys Phe Ser Glu His Tyr His Ser Leu Cys Lys Ala Val
 805 810 815

His His Leu Ala Thr Val Asp Cys Ile Phe Ser Leu Ala Lys Val Ala
 820 825 830

Lys Gln Gly Asp Tyr Cys Arg Pro Thr Val Gln Glu Glu Arg Lys Ile
 835 840 845

Val Ile Lys Asn Gly Arg His Pro Val Ile Asp Val Leu Leu Gly Glu
 850 855 860

Gln Asp Gln Tyr Val Pro Asn Asn Thr Asp Leu Ser Glu Asp Ser Glu
 865 870 875 880

Arg Val Met Ile Ile Thr Gly Pro Asn Met Gly Gly Lys Ser Ser Tyr
 885 890 895

Ile Lys Gln Val Ala Leu Ile Thr Ile Met Ala Gln Ile Gly Ser Tyr
 900 905 910

Val Pro Ala Glu Glu Ala Thr Ile Gly Ile Val Asp Gly Ile Phe Thr
 915 920 925

Arg Met Gly Ala Ala Asp Asn Ile Tyr Lys Gly Arg Ser Thr Phe Met
 930 935 940

Glu Glu Leu Thr Asp Thr Ala Glu Ile Ile Arg Lys Ala Thr Ser Gln
 945 950 955 960

Ser Leu Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr His Asp
 965 970 975

Gly Ile Ala Ile Ala Tyr Ala Thr Leu Glu Tyr Phe Ile Arg Asp Val
 980 985 990

Lys Ser Leu Thr Leu Phe Val Thr His Tyr Pro Pro Val Cys Glu Leu
 995 1000 1005

Glu Lys Asn Tyr Ser His Gln Val Gly Asn Tyr His Met Gly Phe
 1010 1015 1020

Leu Val Ser Glu Asp Glu Ser Lys Leu Asp Pro Gly Ala Ala Glu
 1025 1030 1035

MOR0251.ST25.txt

Gln Val Pro Asp Phe Val Thr Phe Leu Tyr Gln Ile Thr Arg Gly
1040 1045 1050

Ile Ala Ala Arg Ser Tyr Gly Leu Asn Val Ala Lys Leu Ala Asp
1055 1060 1065

Val Pro Gly Glu Ile Leu Lys Lys Ala Ala His Lys Ser Lys Glu
1070 1075 1080

Leu Glu Gly Leu Ile Asn Thr Lys Arg Lys Arg Leu Lys Tyr Phe
1085 1090 1095

Ala Lys Leu Trp Thr Met His Asn Ala Gln Asp Leu Gln Lys Trp
1100 1105 1110

Thr Glu Glu Phe Asn Met Glu Glu Thr Gln Thr Ser Leu Leu His
1115 1120 1125

<210> 19
<211> 3095
<212> DNA
<213> Homo sapiens

<400> 19
cagaaacctc atacttctcg ggtcagggaa ggtttgggag gatgctgagg cctgagatct 60
catcaacctc gccttctgcc ccggcggttt ccccgctcgt cggagaaacc cgctcacctc 120
aggggtccccg ctacaatttc ggactccagg agactccaca gagccgccct tcggtccagg 180
tggtctctgc atccacctgt cctggcacgt caggagctgc gggcgaccgg agcagcagca 240
gcagcagcct tccctgcccc gcgcctaaact cccggccagc tcaaggttca tactttggaa 300
acaaaagagc ttatgcagaa aacacagttg catcaaattt tacttttggg gcaagctcat 360
cttctgcacg agatactaata taccctcaaa cacttaaaac tccattgtct actggaaatc 420
ctcagagatc aggttataag agctggacac cacaagtggg atattcagct tcatcctcat 480
ctgcgatttc tgcacactcc ccatcagtta ttgtagctgt tgtagaaggg agaggacttg 540
ccagaggtga aataggaatg gcaagtattg atttaaaaaa ccccaaatt atactatccc 600
agtttgcaga caacacaaca tatgcaaagg tgatcactaa acttaaaatt ttatcacctt 660
tggaataaat aatgtcaaat actgcttgtg ctgtggggaa ttccaccaag ttgttcactc 720
tgatcacaga aaatttcaag aatgttaatt tcaactactat ccaaaggaaa tacttcaatg 780
aaacaaaagg attaggtac attgaacagt tatgcatagc agaattcagc actgtcctaa 840
tgagaggttca gtccaagtat tactgccttg cagctgttgc agctttgtta aaatatgttg 900
aatttattca aaattcagtt tatgcaccaa aatcactgaa gatttgtttc cagggttagtg 960
aacagacagc catgatagat tcatcatcag cccaaaacct tgaattgtta attaataatc 1020
aagactatag gaataatcac actctctttg gtgttctaaa ttatactaag actcctggag 1080
ggagtagacg acttcgttct aatatattag agcctctagt tgatattgaa accattaaca 1140
tgcgcttaga ttgtgttcaa gaactacttc aagatgagga actatTTTTT ggacttcaat 1200

MOR0251.ST25.txt

cagttatatc aagatttctt gatacagagc agcttccttc tgtttttagtc caaattccag 1260
 agcaagacac ggtcaatgct gctgaatcaa agataacaaa tttaatatatac ttaaaacata 1320
 ccttggaact tgtggatcct ttaaagattg ctatgaagaa ctgtaacaca cctttattaa 1380
 gagcttacta tgggttccttg gaagacaaga ggtttggaat cataacttgaa aagattaaaa 1440
 cagtaattaa tgatgatgca agatacatga aaggatgcct aaacatgagg actcagaagt 1500
 gctatgcagt gaggtctaac ataatgaat ttcttgacat agcaagaaga acatacacag 1560
 agattgtaga tgacatagca ggaatgatata cacaacttgg agaaaaatat agtctacctt 1620
 taaggacaag tcttagctct gtctgaggat ttttcatcca gatgactaca gattgtatag 1680
 ccctacctag tgatcaactt ccttcagaat ttattaagat ttctaaagtg aaaaattctt 1740
 acagctttac atcagcagat ttaattaaaa tgaatgaaag atgccaagaa tctttgagag 1800
 aaatctatca catgacttat atgatagtgt gcaaactgct tagtgagatt tatgaacata 1860
 ttcatgtctt atataaacta tctgacactg tgtcaatgct ggatatgcta ctgtcatttg 1920
 ctcatgcctg cactctttct gactatgttc gaccagaatt tactgatact ttagcaatca 1980
 aacagggatg gcctcctatt cttgaaaaaa tatctgcgga aaaacctatt gccacaata 2040
 cctatgttac agaagggagt aatTTTTTga tcataactgg accaaacatg agtggaaaat 2100
 ccacatattt aaaacagatt gctctttgtc agattatggc ccagattgga tcatatgttc 2160
 cagcagaata ttcttccttt agaattgcta aacagatttt tacaagaatt agtactgatg 2220
 atgatatcga aacaaattca tcaacattta tgaaagaaat gaaagagata gcatatatc 2280
 tacataatgc taatgacaaa tcgctcatat taattgatga acttggcaga ggtactaata 2340
 cggaagaagg tattggcatt tgttatgctg tttgtgaata tctactgagc ttaaaggcat 2400
 ttacactggt tgctacacat ttcttggaa c tatgccatat tgatgccctg tctcctaag 2460
 tagaaaacat gcattttgaa gttcaacatg taaagaatac ctcaagaaat aaagaagcaa 2520
 ttttgtatac ctacaaactt tctaaggac tcacagaaga gaaaaattat ggattaaaag 2580
 ctgcagaggt gtcactcatt ccaccatcaa ttgtcttggg tgccaaggaa atcacaaactc 2640
 aaattacgag acaaatTTtg caaaaccaa ggagtacccc tgagatggaa agacagagag 2700
 ctgtgtacca tctagccact aggcttgttc aaactgctcg aaactctcaa ttggatccag 2760
 acagtttacg aatatattta agtaacctca agaagaagta caaagaagat tttcccagga 2820
 ccgaacaagt tccagaaaag actgaagaat aatcacaatt ctaatgtaat aatatatctt 2880
 aattcaagga acctagaatt tatttttctc cttagagata aggaaaataa catttgccaa 2940
 atttcatatt ttaattgaaa attacattat attaacatca caattgtcat ctatatattc 3000
 tatatgaaaa atatttatta taacttaaca aatgagaact acttaaagga atggttttta 3060
 tgttaggaga aaatacaata caccacaaaa aaaaa 3095

<210> 20
 <211> 936
 <212> PRT
 <213> Homo sapiens

<400> 20

Met Leu Arg Pro Glu Ile Ser Ser Thr Ser Pro Ser Ala Pro Ala Val
 1 5 10 15

Ser Pro Val Val Gly Glu Thr Arg Ser Pro Gln Gly Pro Arg Tyr Asn
 20 25 30

Phe Gly Leu Gln Glu Thr Pro Gln Ser Arg Pro Ser Val Gln Val Val
 35 40 45

Ser Ala Ser Thr Cys Pro Gly Thr Ser Gly Ala Ala Gly Asp Arg Ser
 50 55 60

Ser Ser Ser Ser Ser Leu Pro Cys Pro Ala Pro Asn Ser Arg Pro Ala
 65 70 75 80

Gln Gly Ser Tyr Phe Gly Asn Lys Arg Ala Tyr Ala Glu Asn Thr Val
 85 90 95

Ala Ser Asn Phe Thr Phe Gly Ala Ser Ser Ser Ser Ala Arg Asp Thr
 100 105 110

Asn Tyr Pro Gln Thr Leu Lys Thr Pro Leu Ser Thr Gly Asn Pro Gln
 115 120 125

Arg Ser Gly Tyr Lys Ser Trp Thr Pro Gln Val Gly Tyr Ser Ala Ser
 130 135 140

Ser Ser Ser Ala Ile Ser Ala His Ser Pro Ser Val Ile Val Ala Val
 145 150 155 160

Val Glu Gly Arg Gly Leu Ala Arg Gly Glu Ile Gly Met Ala Ser Ile
 165 170 175

Asp Leu Lys Asn Pro Gln Ile Ile Leu Ser Gln Phe Ala Asp Asn Thr
 180 185 190

Thr Tyr Ala Lys Val Ile Thr Lys Leu Lys Ile Leu Ser Pro Leu Glu
 195 200 205

Ile Ile Met Ser Asn Thr Ala Cys Ala Val Gly Asn Ser Thr Lys Leu
 210 215 220

Phe Thr Leu Ile Thr Glu Asn Phe Lys Asn Val Asn Phe Thr Thr Ile
 225 230 235 240

Gln Arg Lys Tyr Phe Asn Glu Thr Lys Gly Leu Glu Tyr Ile Glu Gln
 245 250 255

Leu Cys Ile Ala Glu Phe Ser Thr Val Leu Met Glu Val Gln Ser Lys
 260 265 270

Tyr Tyr Cys Leu Ala Ala Val Ala Ala Leu Leu Lys Tyr Val Glu Phe
 275 280 285
 Ile Gln Asn Ser Val Tyr Ala Pro Lys Ser Leu Lys Ile Cys Phe Gln
 290 295 300
 Gly Ser Glu Gln Thr Ala Met Ile Asp Ser Ser Ser Ala Gln Asn Leu
 305 310 315 320
 Glu Leu Leu Ile Asn Asn Gln Asp Tyr Arg Asn Asn His Thr Leu Phe
 325 330 335
 Gly Val Leu Asn Tyr Thr Lys Thr Pro Gly Gly Ser Arg Arg Leu Arg
 340 345 350
 Ser Asn Ile Leu Glu Pro Leu Val Asp Ile Glu Thr Ile Asn Met Arg
 355 360 365
 Leu Asp Cys Val Gln Glu Leu Leu Gln Asp Glu Glu Leu Phe Phe Gly
 370 375 380
 Leu Gln Ser Val Ile Ser Arg Phe Leu Asp Thr Glu Gln Leu Leu Ser
 385 390 395 400
 Val Leu Val Gln Ile Pro Glu Gln Asp Thr Val Asn Ala Ala Glu Ser
 405 410 415
 Lys Ile Thr Asn Leu Ile Tyr Leu Lys His Thr Leu Glu Leu Val Asp
 420 425 430
 Pro Leu Lys Ile Ala Met Lys Asn Cys Asn Thr Pro Leu Leu Arg Ala
 435 440 445
 Tyr Tyr Gly Ser Leu Glu Asp Lys Arg Phe Gly Ile Ile Leu Glu Lys
 450 455 460
 Ile Lys Thr Val Ile Asn Asp Asp Ala Arg Tyr Met Lys Gly Cys Leu
 465 470 475 480
 Asn Met Arg Thr Gln Lys Cys Tyr Ala Val Arg Ser Asn Ile Asn Glu
 485 490 495
 Phe Leu Asp Ile Ala Arg Arg Thr Tyr Thr Glu Ile Val Asp Asp Ile
 500 505 510
 Ala Gly Met Ile Ser Gln Leu Gly Glu Lys Tyr Ser Leu Pro Leu Arg
 515 520 525
 Thr Ser Leu Ser Ser Val Arg Gly Phe Phe Ile Gln Met Thr Thr Asp
 530 535 540
 Cys Ile Ala Leu Pro Ser Asp Gln Leu Pro Ser Glu Phe Ile Lys Ile
 545 550 555 560

Ser Lys Val Lys Asn Ser Tyr Ser Phe Thr Ser Ala Asp Leu Ile Lys
 565 570 575
 Met Asn Glu Arg Cys Gln Glu Ser Leu Arg Glu Ile Tyr His Met Thr
 580 585 590
 Tyr Met Ile Val Cys Lys Leu Leu Ser Glu Ile Tyr Glu His Ile His
 595 600 605
 Cys Leu Tyr Lys Leu Ser Asp Thr Val Ser Met Leu Asp Met Leu Leu
 610 615 620
 Ser Phe Ala His Ala Cys Thr Leu Ser Asp Tyr Val Arg Pro Glu Phe
 625 630 635 640
 Thr Asp Thr Leu Ala Ile Lys Gln Gly Trp His Pro Ile Leu Glu Lys
 645 650 655
 Ile Ser Ala Glu Lys Pro Ile Ala Asn Asn Thr Tyr Val Thr Glu Gly
 660 665 670
 Ser Asn Phe Leu Ile Ile Thr Gly Pro Asn Met Ser Gly Lys Ser Thr
 675 680 685
 Tyr Leu Lys Gln Ile Ala Leu Cys Gln Ile Met Ala Gln Ile Gly Ser
 690 695 700
 Tyr Val Pro Ala Glu Tyr Ser Ser Phe Arg Ile Ala Lys Gln Ile Phe
 705 710 715 720
 Thr Arg Ile Ser Thr Asp Asp Asp Ile Glu Thr Asn Ser Ser Thr Phe
 725 730 735
 Met Lys Glu Met Lys Glu Ile Ala Tyr Ile Leu His Asn Ala Asn Asp
 740 745 750
 Lys Ser Leu Ile Leu Ile Asp Glu Leu Gly Arg Gly Thr Asn Thr Glu
 755 760 765
 Glu Gly Ile Gly Ile Cys Tyr Ala Val Cys Glu Tyr Leu Leu Ser Leu
 770 775 780
 Lys Ala Phe Thr Leu Phe Ala Thr His Phe Leu Glu Leu Cys His Ile
 785 790 795 800
 Asp Ala Leu Tyr Pro Asn Val Glu Asn Met His Phe Glu Val Gln His
 805 810 815
 Val Lys Asn Thr Ser Arg Asn Lys Glu Ala Ile Leu Tyr Thr Tyr Lys
 820 825 830

MOR0251.ST25.txt

Leu Ser Lys Gly Leu Thr Glu Glu Lys Asn Tyr Gly Leu Lys Ala Ala
 835 840 845

Glu Val Ser Ser Leu Pro Pro Ser Ile Val Leu Asp Ala Lys Glu Ile
 850 855 860

Thr Thr Gln Ile Thr Arg Gln Ile Leu Gln Asn Gln Arg Ser Thr Pro
 865 870 875 880

Glu Met Glu Arg Gln Arg Ala Val Tyr His Leu Ala Thr Arg Leu Val
 885 890 895

Gln Thr Ala Arg Asn Ser Gln Leu Asp Pro Asp Ser Leu Arg Ile Tyr
 900 905 910

Leu Ser Asn Leu Lys Lys Lys Tyr Lys Glu Asp Phe Pro Arg Thr Glu
 915 920 925

Gln Val Pro Glu Lys Thr Glu Glu
 930 935

<210> 21
 <211> 2726
 <212> DNA
 <213> Homo sapiens

<400> 21
 gcggtcggtc agcggggcgt tctccacact gtagcgactc agagcctcca agctcatggc 60
 ctccttagga gcgaacccaa ggaggacacc gcagggaccg agacctgggg cggcctcctc 120
 cggcttcccc agcccggccc cagtgccggg cccagggag gccgaggagg aggaagtoga 180
 ggaggaggag gagctggccg agatccatct gtgtgtgctg tggaattcag gatacttggg 240
 cattgcctac tatgatacta gtgactccac tatccacttc atgccagatg cccagacca 300
 cgagagcctc aagcttctcc agagagttct ggatgagatc aatccccagt ctgttggtac 360
 gagtgccaaa caggatgaga atatgactcg atttctggga aagcttgctt cccaggagca 420
 cagagagcct aaaagacctg aaatcatatt tttgccaagt gtggattttg gtctggagat 480
 aagcaaacia cgcttccttt ctggaaacta ctccttcac cagacgcca tgactgccac 540
 tgagaaaatc ctcttcctct cttccattat tccctttgac tgcctcctca cagttcgagc 600
 acttgagggg ctgctgaagt tcctgggtcg aagaagaatc ggggttgaa tggaagacta 660
 taatgtcagc gtccccatcc tgggctttta gaaatttatg ttgactcatc tggatgaacat 720
 agatcaagac acttacagtg ttctacagat ttttaagagt gagtctcacc cctcagtgtg 780
 caaagtggcc agtggactga aggaggggct cagcctcttt ggaatcctca acagatgcca 840
 ctgtaagtgg ggagagaagc tgctcaggct atggttcaca cgtccgactc atgacctggg 900
 ggagctcagt tctcgtctgg acgtcattca gttttttctg ctgccccaga atctggacat 960
 ggctcagatg ctgcatcggc tcctgggtca catcaagaac gtgcctctga ttctgaaacg 1020
 catgaagttg tccacacca aggtcagcga ctggcaggtt ctctacaaga ctgtgtacag 1080

MOR0251.ST25.txt

```

tgccctgggc ctgagggatg cctgccgctc cctgccgcag tccatccagc tctttcggga 1140
cattgcccga gagttctctg atgacctgca ccatatcgcc agcctcattg ggaaagtagt 1200
ggactttgag ggcagccttg ctgaaaatcg cttcacagtc ctccccaaca tagatcctga 1260
aattgatgag aaaaagcgaa gactgatggg acttcccagt ttccttactg aggttgcccg 1320
caaggagctg gagaatctgg actcccgtat tccttcatgc agtgtcatct acatccctct 1380
gattggcttc cttcttttcta tccccgcct gccttccatg gtagaggcca gtgactttga 1440
gattaatgga ctggacttca tgtttctctc agaggagaag ctgcactatc gtagtgcccg 1500
aaccaaggag ctggatgcat tgctggggga cctgcactgc gagatccggg accaggagac 1560
gctgctgatg taccagctac agtgccaggt gctggcacga gcagctgtct taacccgagt 1620
attggacctt gcctcccgcc tggacgtcct gctggctctt gccagtgtg cccgggacta 1680
tggctactca aggccgcgtt actccccaca agtccttggg gtacgaatcc agaatggcag 1740
acatcctctg atggaactct gtgcccgaac ctttgtgccc aactccacag aatgtggtgg 1800
ggacaaaggg aggggtcaaag tcatcactgg acccaactca tcagggaaga gcatatacct 1860
caaacaggta ggcttgatca cattcatggc cctggtaggc agctttgtgc cagcagagga 1920
ggccgaaatt ggggcagtag acgccatctt cacacgaatt catagctgcg aatccatctc 1980
ccttggcctc tccaccttca tgatcgacct caaccagcag gtggcgaaag cagtgaacaa 2040
tgccactgca cagtcgctgg tccttattga tgaatttgga aagggaacca acacggtgga 2100
tgggctcgcg cttctggccg ctgtgctccg aactggctg gcacgtggac ccacatgccc 2160
ccacatcttt gtggccacca actttctgag ccttgttcag ctacaactgc tgccacaagg 2220
gccctggtg cagtatttga ccatggagac ctgtgaggat ggcaacgac ttgtcttctt 2280
ctatcagggt tgcaagggtg ttgcaaggc cagccatgcc tcccacacag ctgcccaggc 2340
tgggcttcct gacaagcttg tggctcgtgg caaggaggtc tcagacttga tccgcagtgg 2400
aaaaccatc aagcctgtca aggatttgc aaagaagaac caaatggaaa attgccagac 2460
attagtggat aagtttatga aactggattt ggaagatcct aacctggact tgaacgtttt 2520
catgagccag gaagtgtgct ctgctgccac cagcatcctc tgagagtctt tccagtgtcc 2580
tccccagcct cctgagactc cggtagggctg ccatgccctc tttgttctt tatctccctc 2640
agacgcagag tttttagttt ctctagaaat tttgtttcat attaggaata aagtttattt 2700
tgaagaaaaa aaaaaaaaaa aaaaaa 2726

```

<210> 22
 <211> 835
 <212> PRT
 <213> Homo sapiens

<400> 22

Met Ala Ser Leu Gly Ala Asn Pro Arg Arg Thr Pro Gln Gly Pro Arg
 1 5 10 15

Pro Gly Ala Ala Ser Ser Gly Phe Pro Ser Pro Ala Pro Val Pro Gly
 20 25 30

Pro Arg Glu Ala Glu Glu Glu Glu Val Glu Glu Glu Glu Glu Leu Ala
 35 40 45
 Glu Ile His Leu Cys Val Leu Trp Asn Ser Gly Tyr Leu Gly Ile Ala
 50 55 60
 Tyr Tyr Asp Thr Ser Asp Ser Thr Ile His Phe Met Pro Asp Ala Pro
 65 70 75 80
 Asp His Glu Ser Leu Lys Leu Leu Gln Arg Val Leu Asp Glu Ile Asn
 85 90 95
 Pro Gln Ser Val Val Thr Ser Ala Lys Gln Asp Glu Asn Met Thr Arg
 100 105 110
 Phe Leu Gly Lys Leu Ala Ser Gln Glu His Arg Glu Pro Lys Arg Pro
 115 120 125
 Glu Ile Ile Phe Leu Pro Ser Val Asp Phe Gly Leu Glu Ile Ser Lys
 130 135 140
 Gln Arg Leu Leu Ser Gly Asn Tyr Ser Phe Ile Pro Asp Ala Met Thr
 145 150 155 160
 Ala Thr Glu Lys Ile Leu Phe Leu Ser Ser Ile Ile Pro Phe Asp Cys
 165 170 175
 Leu Leu Thr Val Arg Ala Leu Gly Gly Leu Leu Lys Phe Leu Gly Arg
 180 185 190
 Arg Arg Ile Gly Val Glu Leu Glu Asp Tyr Asn Val Ser Val Pro Ile
 195 200 205
 Leu Gly Phe Lys Lys Phe Met Leu Thr His Leu Val Asn Ile Asp Gln
 210 215 220
 Asp Thr Tyr Ser Val Leu Gln Ile Phe Lys Ser Glu Ser His Pro Ser
 225 230 235 240
 Val Tyr Lys Val Ala Ser Gly Leu Lys Glu Gly Leu Ser Leu Phe Gly
 245 250 255
 Ile Leu Asn Arg Cys His Cys Lys Trp Gly Glu Lys Leu Leu Arg Leu
 260 265 270
 Trp Phe Thr Arg Pro Thr His Asp Leu Gly Glu Leu Ser Ser Arg Leu
 275 280 285
 Asp Val Ile Gln Phe Phe Leu Leu Pro Gln Asn Leu Asp Met Ala Gln
 290 295 300

MOR0251.ST25.txt

Met Leu His Arg Leu Leu Gly His Ile Lys Asn Val Pro Leu Ile Leu
 305 310 315 320

Lys Arg Met Lys Leu Ser His Thr Lys Val Ser Asp Trp Gln Val Leu
 325 330 335

Tyr Lys Thr Val Tyr Ser Ala Leu Gly Leu Arg Asp Ala Cys Arg Ser
 340 345 350

Leu Pro Gln Ser Ile Gln Leu Phe Arg Asp Ile Ala Gln Glu Phe Ser
 355 360 365

Asp Asp Leu His His Ile Ala Ser Leu Ile Gly Lys Val Val Asp Phe
 370 375 380

Glu Gly Ser Leu Ala Glu Asn Arg Phe Thr Val Leu Pro Asn Ile Asp
 385 390 395 400

Pro Glu Ile Asp Glu Lys Lys Arg Arg Leu Met Gly Leu Pro Ser Phe
 405 410 415

Leu Thr Glu Val Ala Arg Lys Glu Leu Glu Asn Leu Asp Ser Arg Ile
 420 425 430

Pro Ser Cys Ser Val Ile Tyr Ile Pro Leu Ile Gly Phe Leu Leu Ser
 435 440 445

Ile Pro Arg Leu Pro Ser Met Val Glu Ala Ser Asp Phe Glu Ile Asn
 450 455 460

Gly Leu Asp Phe Met Phe Leu Ser Glu Glu Lys Leu His Tyr Arg Ser
 465 470 475 480

Ala Arg Thr Lys Glu Leu Asp Ala Leu Leu Gly Asp Leu His Cys Glu
 485 490 495

Ile Arg Asp Gln Glu Thr Leu Leu Met Tyr Gln Leu Gln Cys Gln Val
 500 505 510

Leu Ala Arg Ala Ala Val Leu Thr Arg Val Leu Asp Leu Ala Ser Arg
 515 520 525

Leu Asp Val Leu Leu Ala Leu Ala Ser Ala Ala Arg Asp Tyr Gly Tyr
 530 535 540

Ser Arg Pro Arg Tyr Ser Pro Gln Val Leu Gly Val Arg Ile Gln Asn
 545 550 555 560

Gly Arg His Pro Leu Met Glu Leu Cys Ala Arg Thr Phe Val Pro Asn
 565 570 575

Ser Thr Glu Cys Gly Gly Asp Lys Gly Arg Val Lys Val Ile Thr Gly
 580 585 590

Pro Asn Ser Ser Gly Lys Ser Ile Tyr Leu Lys Gln Val Gly Leu Ile
595 600 605

Thr Phe Met Ala Leu Val Gly Ser Phe Val Pro Ala Glu Glu Ala Glu
610 615 620

Ile Gly Ala Val Asp Ala Ile Phe Thr Arg Ile His Ser Cys Glu Ser
625 630 635 640

Ile Ser Leu Gly Leu Ser Thr Phe Met Ile Asp Leu Asn Gln Gln Val
645 650 655

Ala Lys Ala Val Asn Asn Ala Thr Ala Gln Ser Leu Val Leu Ile Asp
660 665 670

Glu Phe Gly Lys Gly Thr Asn Thr Val Asp Gly Leu Ala Leu Leu Ala
675 680 685

Ala Val Leu Arg His Trp Leu Ala Arg Gly Pro Thr Cys Pro His Ile
690 695 700

Phe Val Ala Thr Asn Phe Leu Ser Leu Val Gln Leu Gln Leu Leu Pro
705 710 715 720

Gln Gly Pro Leu Val Gln Tyr Leu Thr Met Glu Thr Cys Glu Asp Gly
725 730 735

Asn Asp Leu Val Phe Phe Tyr Gln Val Cys Glu Gly Val Ala Lys Ala
740 745 750

Ser His Ala Ser His Thr Ala Ala Gln Ala Gly Leu Pro Asp Lys Leu
755 760 765

Val Ala Arg Gly Lys Glu Val Ser Asp Leu Ile Arg Ser Gly Lys Pro
770 775 780

Ile Lys Pro Val Lys Asp Leu Leu Lys Lys Asn Gln Met Glu Asn Cys
785 790 795 800

Gln Thr Leu Val Asp Lys Phe Met Lys Leu Asp Leu Glu Asp Pro Asn
805 810 815

Leu Asp Leu Asn Val Phe Met Ser Gln Glu Val Leu Pro Ala Ala Thr
820 825 830

Ser Ile Leu
835

<210> 23
<211> 4264
<212> DNA
<213> Homo sapiens

```

<400> 23
atttcccgcc agcaggagcc ggcgggtaga tgcggtgctt ttaggagctc cgtccgacag      60
aacggttggg ccttgccggc tgcggtatg tcgcgacaga gcacctgta cagcttcttc      120
cccaagtctc cggcgctgag tgatgccaac aaggcctcgg ccagggcctc acgcgaaggc      180
ggcctgccc cgcgtgcccc cggggcctct ccttccccag gcggggatgc ggcttgagc      240
gaggctgggc ctggggccag gcccttggcg cgatccgcgt caccgcccaa ggcgaagaac      300
ctcaacggag ggctgcggag atcggtagcg cctgctgccc ccaccagttg tgactttctca      360
ccaggagatt tggtttgggc caagatggag ggttaccctt ggtggccttg tctggtttac      420
aaccaccctt ttgatggaac attcatccgc gagaaagga aatcagtcgg tgttcatgta      480
cagttttttg atgacagccc aacaaggggc tgggttagca aaaggctttt aaagccatat      540
acaggttcaa aatcaaagga agcccagaag ggaggtcatt tttacagtgc aaagcctgaa      600
atactgagag caatgcaacg tgcagatgaa gccttaaata aagacaagat taagaggctt      660
gaattggcag tttgtgatga gccctcagag ccagaagagg aagaagagat ggaggtaggc      720
acaacttacg taacagataa gagtgaagaa gataatgaaa ttgagagtga agaggaagta      780
cagcctaaga cacaaggatc taggcgaagt agccgccaaa taaaaaacg aagggtcata      840
tcagattctg agagtgcacat tgggtggctct gatgtggaat ttaagccaga cactaaggag      900
gaaggaagca gtgatgaaat aagcagtgga gtgggggata gtgagagtga aggctgaac      960
agccctgtca aagttgctcg aaagcggaag agaatggtga ctggaaatgg ctctcttaaa     1020
agggaaagct ctaggaagga aacgcctca gccacaaac aagcaactag catttcatca     1080
gaaaccaaga atactttgag agctttctct gccctcaaa attctgaatc ccaagcccac     1140
gttagtgagg gtggtgatga cagtagtcgc cctactgttt ggtatcatga aactttagaa     1200
tggcttaagg agggaaagag aagagatgag cacaggagga ggctgatca ccccgatttt     1260
gatgcatcta cactctatgt gcctgaggat ttctcaatt cttgtactcc tgggatgagg     1320
aagtgggtgg agattaagtc tcagaacttt gatcttgtca tctgttaca ggtggggaaa     1380
ttttatgagc tgtaccacat ggatgctctt attggagtca gtgaactggg gctggtattc     1440
atgaaaggca actgggcca ttctggcttt cctgaaattg catttgccg ttattcagat     1500
tcctgggtgc agaagggcta taaagtagca cgagtggaac agactgagac tccagaaatg     1560
atggaggcac gatgtagaaa gatggcacat atatccaagt atgatagagt ggtgaggagg     1620
gagatctgta ggatcattac caagggtaca cagacttaca gtgtgctgga aggtgatccc     1680
tctgagaact acagtaagta tcttcttagc ctcaaagaaa aagaggaaga ttcttctggc     1740
catactcgtg catatggtgt gtgctttggt gatacttcac tgggaaagtt tttcataggt     1800
cagttttcag atgatcgcca ttgttcgaga tttaggactc tagtggcaca ctatcccca     1860
gtacaagttt tatttgaaaa aggaaatctc tcaaaggaaa ctaaaacaat tctaaagagt     1920
tcattgtcct gttctcttca ggaaggctct ataccggct ccagttttg ggatgcatcc     1980
aaaactttga gaactctcct tgaggaagaa tatttttagg aaaagctaag tgatggcatt     2040

```


MOR0251.ST25.txt

ggggtgatgt taccacaggt gcttaaaggt atgacttcag agtctgattc cattgggttg 2100
 acaccaggag agaaaagtga attggccctc tctgctctag gtggttgtgt cttctacctc 2160
 aaaaaatgcc ttattgatca ggagctttta tcaatggcta attttgaaga atatatccc 2220
 ttgattctg acacagtcag cactacaaga tctggtgcta tcttcaccaa agcctatcaa 2280
 cgaatggtgc tagatgcagt gacattaaac aacttggaga tttttctgaa tggaacaaat 2340
 ggttctactg aaggaaccct actagagagg gttgatactt gccatactcc ttttggttaag 2400
 cggctcctaa agcaatggct ttgtgcccc aactgttaacc attatgctat taatgatcgt 2460
 ctagatgcc tagaagacct catggttgtg cctgacaaaa tctccgaagt tgtagagctt 2520
 ctaaagaagc ttccagatct tgagaggcta ctacagtaaaa ttcataatgt tgggtctccc 2580
 ctgaagagtc agaaccaccc agacagcagg gctataatgt atgaagaaac tacatacagc 2640
 aagaagaaga ttattgattt tctttctgct ctggaaggat tcaaagtaat gtgtaaaatt 2700
 atagggatca tggaagaagt tgctgatggt ttttaagtcta aaatccttaa gcaggtcac 2760
 tctctgcaga caaaaaatcc tgaaggctgt tttcctgatt tgactgtaga attgaaccga 2820
 tgggatacag cttttgacca tgaaaaggct cgaaagactg gacttattac tcccaaagca 2880
 ggctttgact ctgattatga ccaagctctt gctgacataa gagaaaatga acagagcctc 2940
 ctggaatacc tagagaaaca gcgcaacaga attggctgta ggaccatagt ctattggggg 3000
 attggtagga accgttacca gctggaaatt cctgagaatt tcaccactcg caatttgcca 3060
 gaagaatacg agttgaaatc taccaagaag ggctgtaaac gatactggac caaaactatt 3120
 gaaaagaagt tggctaattc cataaatgct gaagaacgga gggatgtatc attgaaggac 3180
 tgcatgcggc gactgttcta taactttgat aaaaattaca aggactggca gtctgctgta 3240
 gagtgtatcg cagtgttga tggtttactg tgccctggcta actatagtcg agggggtgat 3300
 ggtcctatgt gtcgccaggt aattctgttg ccggaagata cccccctt cttagagctt 3360
 aaaggatcac gccatccttg cattacgaag acttttttg gagatgattt tttcctaatt 3420
 gacattctaa taggctgtga ggaagaggag caggaaaatg gcaaagccta ttgtgtgctt 3480
 gttactggac caaatatggg gggcaagtct acgcttatga gacaggctgg cttattagct 3540
 gtaatggccc agatgggttg ttacgtccct gctgaagtgt gcaggctcac accaattgat 3600
 agagtgttta ctagacttgg tgcctcagac agaataatgt caggtgaaag tacatTTTTT 3660
 gttgaattaa gtgaaactgc cagcactc atgcatgcaa cagcacattc tctggtgctt 3720
 gtggatgaat taggaagagg tactgcaaca tttgatggga cggcaatagc aaatgcagtt 3780
 gttaaagaac ttgctgagac tataaaatgt cgtacattat tttcaactca ctaccattca 3840
 ttagtagaag attattctca aaatgttgct gtgcgcctag gacatatggc atgcatggta 3900
 gaaaatgaat gtgaagaccc cagccaggag actattacgt tcctctataa attcattaag 3960
 ggagcttgtc ctaaaagcta tggctttaat gcagcaaggc ttgctaattc ccagaggaa 4020
 gttattcaaa agggacatag aaaagcaaga gaatttgaga agatgaatca gtcactacga 4080
 ttatttcggg aagtttgcct ggctagtga aggtcaactg tagatgctga agctgtccat 4140

MOR0251.ST25.txt

aaattgctga ctttgattaa ggaattatag actgactaca ttggaagctt tgagttgact 4200
 tctgaccaaa ggtggtaaatt tcagacaaca ttatgatcta ataaacttta ttttttaaaa 4260
 atga 4264

<210> 24
 <211> 1360
 <212> PRT
 <213> Homo sapiens

<400> 24

Met Ser Arg Gln Ser Thr Leu Tyr Ser Phe Phe Pro Lys Ser Pro Ala
 1 5 10 15

Leu Ser Asp Ala Asn Lys Ala Ser Ala Arg Ala Ser Arg Glu Gly Gly
 20 25 30

Arg Ala Ala Ala Ala Pro Gly Ala Ser Pro Ser Pro Gly Gly Asp Ala
 35 40 45

Ala Trp Ser Glu Ala Gly Pro Gly Pro Arg Pro Leu Ala Arg Ser Ala
 50 55 60

Ser Pro Pro Lys Ala Lys Asn Leu Asn Gly Gly Leu Arg Arg Ser Val
 65 70 75 80

Ala Pro Ala Ala Pro Thr Ser Cys Asp Phe Ser Pro Gly Asp Leu Val
 85 90 95

Trp Ala Lys Met Glu Gly Tyr Pro Trp Trp Pro Cys Leu Val Tyr Asn
 100 105 110

His Pro Phe Asp Gly Thr Phe Ile Arg Glu Lys Gly Lys Ser Val Arg
 115 120 125

Val His Val Gln Phe Phe Asp Asp Ser Pro Thr Arg Gly Trp Val Ser
 130 135 140

Lys Arg Leu Leu Lys Pro Tyr Thr Gly Ser Lys Ser Lys Glu Ala Gln
 145 150 155 160

Lys Gly Gly His Phe Tyr Ser Ala Lys Pro Glu Ile Leu Arg Ala Met
 165 170 175

Gln Arg Ala Asp Glu Ala Leu Asn Lys Asp Lys Ile Lys Arg Leu Glu
 180 185 190

Leu Ala Val Cys Asp Glu Pro Ser Glu Pro Glu Glu Glu Glu Met
 195 200 205

Glu Val Gly Thr Thr Tyr Val Thr Asp Lys Ser Glu Glu Asp Asn Glu
 210 215 220

MOR0251.ST25.txt

Ile Glu Ser Glu Glu Glu Val Gln Pro Lys Thr Gln Gly Ser Arg Arg
 225 230 235 240

Ser Ser Arg Gln Ile Lys Lys Arg Arg Val Ile Ser Asp Ser Glu Ser
 245 250 255

Asp Ile Gly Gly Ser Asp Val Glu Phe Lys Pro Asp Thr Lys Glu Glu
 260 265 270

Gly Ser Ser Asp Glu Ile Ser Ser Gly Val Gly Asp Ser Glu Ser Glu
 275 280 285

Gly Leu Asn Ser Pro Val Lys Val Ala Arg Lys Arg Lys Arg Met Val
 290 295 300

Thr Gly Asn Gly Ser Leu Lys Arg Lys Ser Ser Arg Lys Glu Thr Pro
 305 310 315 320

Ser Ala Thr Lys Gln Ala Thr Ser Ile Ser Ser Glu Thr Lys Asn Thr
 325 330 335

Leu Arg Ala Phe Ser Ala Pro Gln Asn Ser Glu Ser Gln Ala His Val
 340 345 350

Ser Gly Gly Gly Asp Asp Ser Ser Arg Pro Thr Val Trp Tyr His Glu
 355 360 365

Thr Leu Glu Trp Leu Lys Glu Glu Lys Arg Arg Asp Glu His Arg Arg
 370 375 380

Arg Pro Asp His Pro Asp Phe Asp Ala Ser Thr Leu Tyr Val Pro Glu
 385 390 395 400

Asp Phe Leu Asn Ser Cys Thr Pro Gly Met Arg Lys Trp Trp Gln Ile
 405 410 415

Lys Ser Gln Asn Phe Asp Leu Val Ile Cys Tyr Lys Val Gly Lys Phe
 420 425 430

Tyr Glu Leu Tyr His Met Asp Ala Leu Ile Gly Val Ser Glu Leu Gly
 435 440 445

Leu Val Phe Met Lys Gly Asn Trp Ala His Ser Gly Phe Pro Glu Ile
 450 455 460

Ala Phe Gly Arg Tyr Ser Asp Ser Leu Val Gln Lys Gly Tyr Lys Val
 465 470 475 480

Ala Arg Val Glu Gln Thr Glu Thr Pro Glu Met Met Glu Ala Arg Cys
 485 490 495

Arg Lys Met Ala His Ile Ser Lys Tyr Asp Arg Val Val Arg Arg Glu
 500 505 510

```

Ile Cys Arg Ile Ile Thr Lys Gly Thr Gln Thr Tyr Ser Val Leu Glu
515                               520                               525

Gly Asp Pro Ser Glu Asn Tyr Ser Lys Tyr Leu Leu Ser Leu Lys Glu
530                               535                               540

Lys Glu Glu Asp Ser Ser Gly His Thr Arg Ala Tyr Gly Val Cys Phe
545                               550                               555                               560

Val Asp Thr Ser Leu Gly Lys Phe Phe Ile Gly Gln Phe Ser Asp Asp
565                               570                               575

Arg His Cys Ser Arg Phe Arg Thr Leu Val Ala His Tyr Pro Pro Val
580                               585                               590

Gln Val Leu Phe Glu Lys Gly Asn Leu Ser Lys Glu Thr Lys Thr Ile
595                               600                               605

Leu Lys Ser Ser Leu Ser Cys Ser Leu Gln Glu Gly Leu Ile Pro Gly
610                               615                               620

Ser Gln Phe Trp Asp Ala Ser Lys Thr Leu Arg Thr Leu Leu Glu Glu
625                               630                               635                               640

Glu Tyr Phe Arg Glu Lys Leu Ser Asp Gly Ile Gly Val Met Leu Pro
645                               650                               655

Gln Val Leu Lys Gly Met Thr Ser Glu Ser Asp Ser Ile Gly Leu Thr
660                               665                               670

Pro Gly Glu Lys Ser Glu Leu Ala Leu Ser Ala Leu Gly Gly Cys Val
675                               680                               685

Phe Tyr Leu Lys Lys Cys Leu Ile Asp Gln Glu Leu Leu Ser Met Ala
690                               695                               700

Asn Phe Glu Glu Tyr Ile Pro Leu Asp Ser Asp Thr Val Ser Thr Thr
705                               710                               715                               720

Arg Ser Gly Ala Ile Phe Thr Lys Ala Tyr Gln Arg Met Val Leu Asp
725                               730                               735

Ala Val Thr Leu Asn Asn Leu Glu Ile Phe Leu Asn Gly Thr Asn Gly
740                               745                               750

Ser Thr Glu Gly Thr Leu Leu Glu Arg Val Asp Thr Cys His Thr Pro
755                               760                               765

Phe Gly Lys Arg Leu Leu Lys Gln Trp Leu Cys Ala Pro Leu Cys Asn
770                               775                               780

```

MOR0251.ST25.txt

His Tyr Ala Ile Asn Asp Arg Leu Asp Ala Ile Glu Asp Leu Met Val
 785 790 795 800

Val Pro Asp Lys Ile Ser Glu Val Val Glu Leu Leu Lys Lys Leu Pro
 805 810 815

Asp Leu Glu Arg Leu Leu Ser Lys Ile His Asn Val Gly Ser Pro Leu
 820 825 830

Lys Ser Gln Asn His Pro Asp Ser Arg Ala Ile Met Tyr Glu Glu Thr
 835 840 845

Thr Tyr Ser Lys Lys Lys Ile Ile Asp Phe Leu Ser Ala Leu Glu Gly
 850 855 860

Phe Lys Val Met Cys Lys Ile Ile Gly Ile Met Glu Glu Val Ala Asp
 865 870 875 880

Gly Phe Lys Ser Lys Ile Leu Lys Gln Val Ile Ser Leu Gln Thr Lys
 885 890 895

Asn Pro Glu Gly Arg Phe Pro Asp Leu Thr Val Glu Leu Asn Arg Trp
 900 905 910

Asp Thr Ala Phe Asp His Glu Lys Ala Arg Lys Thr Gly Leu Ile Thr
 915 920 925

Pro Lys Ala Gly Phe Asp Ser Asp Tyr Asp Gln Ala Leu Ala Asp Ile
 930 935 940

Arg Glu Asn Glu Gln Ser Leu Leu Glu Tyr Leu Glu Lys Gln Arg Asn
 945 950 955 960

Arg Ile Gly Cys Arg Thr Ile Val Tyr Trp Gly Ile Gly Arg Asn Arg
 965 970 975

Tyr Gln Leu Glu Ile Pro Glu Asn Phe Thr Thr Arg Asn Leu Pro Glu
 980 985 990

Glu Tyr Glu Leu Lys Ser Thr Lys Lys Gly Cys Lys Arg Tyr Trp Thr
 995 1000 1005

Lys Thr Ile Glu Lys Lys Leu Ala Asn Leu Ile Asn Ala Glu Glu
 1010 1015 1020

Arg Arg Asp Val Ser Leu Lys Asp Cys Met Arg Arg Leu Phe Tyr
 1025 1030 1035

Asn Phe Asp Lys Asn Tyr Lys Asp Trp Gln Ser Ala Val Glu Cys
 1040 1045 1050

Ile Ala Val Leu Asp Val Leu Leu Cys Leu Ala Asn Tyr Ser Arg
 1055 1060 1065

Gly	Gly	Asp	Gly	Pro	Met	Cys	Arg	Pro	Val	Ile	Leu	Leu	Pro	Glu
	1070					1075					1080			
Asp	Thr	Pro	Pro	Phe	Leu	Glu	Leu	Lys	Gly	Ser	Arg	His	Pro	Cys
	1085					1090					1095			
Ile	Thr	Lys	Thr	Phe	Phe	Gly	Asp	Asp	Phe	Ile	Pro	Asn	Asp	Ile
	1100					1105					1110			
Leu	Ile	Gly	Cys	Glu	Glu	Glu	Glu	Gln	Glu	Asn	Gly	Lys	Ala	Tyr
	1115					1120					1125			
Cys	Val	Leu	Val	Thr	Gly	Pro	Asn	Met	Gly	Gly	Lys	Ser	Thr	Leu
	1130					1135					1140			
Met	Arg	Gln	Ala	Gly	Leu	Leu	Ala	Val	Met	Ala	Gln	Met	Gly	Cys
	1145					1150					1155			
Tyr	Val	Pro	Ala	Glu	Val	Cys	Arg	Leu	Thr	Pro	Ile	Asp	Arg	Val
	1160					1165					1170			
Phe	Thr	Arg	Leu	Gly	Ala	Ser	Asp	Arg	Ile	Met	Ser	Gly	Glu	Ser
	1175					1180					1185			
Thr	Phe	Phe	Val	Glu	Leu	Ser	Glu	Thr	Ala	Ser	Ile	Leu	Met	His
	1190					1195					1200			
Ala	Thr	Ala	His	Ser	Leu	Val	Leu	Val	Asp	Glu	Leu	Gly	Arg	Gly
	1205					1210					1215			
Thr	Ala	Thr	Phe	Asp	Gly	Thr	Ala	Ile	Ala	Asn	Ala	Val	Val	Lys
	1220					1225					1230			
Glu	Leu	Ala	Glu	Thr	Ile	Lys	Cys	Arg	Thr	Leu	Phe	Ser	Thr	His
	1235					1240					1245			
Tyr	His	Ser	Leu	Val	Glu	Asp	Tyr	Ser	Gln	Asn	Val	Ala	Val	Arg
	1250					1255					1260			
Leu	Gly	His	Met	Ala	Cys	Met	Val	Glu	Asn	Glu	Cys	Glu	Asp	Pro
	1265					1270					1275			
Ser	Gln	Glu	Thr	Ile	Thr	Phe	Leu	Tyr	Lys	Phe	Ile	Lys	Gly	Ala
	1280					1285					1290			
Cys	Pro	Lys	Ser	Tyr	Gly	Phe	Asn	Ala	Ala	Arg	Leu	Ala	Asn	Leu
	1295					1300					1305			
Pro	Glu	Glu	Val	Ile	Gln	Lys	Gly	His	Arg	Lys	Ala	Arg	Glu	Phe
	1310					1315					1320			

Glu Lys Met Asn Gln Ser Leu Arg Leu Phe Arg Glu Val Cys Leu
 1325 1330 1335

Ala Ser Glu Arg Ser Thr Val Asp Ala Glu Ala Val His Lys Leu
 1340 1345 1350

Leu Thr Leu Ile Lys Glu Leu
 1355 1360

<210> 25
 <211> 1445
 <212> DNA
 <213> Homo sapiens

<400> 25
 tttttttttt tgatgttctc cagtgcctca gtggcagcag aactggccct gtatcaggcc 60
 gctaccgccca ctccatgacc aacctccctg catacccccc cccccagcac ccctcccaca 120
 ggaccgcttc tgtgttttggg acccaccagg cctttgcacc atacaacaaa ccctcactct 180
 ccggggcccg gtctgcgccc aggetgaaca ccacgaacgc ctgggacgca gctcctcctt 240
 ccctggggag ccagcccctc taccgtctca gcctctccca cctgggacgg cagcacctgc 300
 ccccaggatc ctccacctcc ggtgcagtca gtgcctccct ccccagcggg ccctcaagca 360
 gcccaggcga gcgtccctgc cactgtgccc atgcagatgc caagccagca gagtcagcag 420
 gcgctcgctg gagcgacccg aagccagagc agagcagagc aggtcataaa actacacgga 480
 agagctgaaa gtgccccag atgaggactg catcatctgc atggagaagc tgtccgcagc 540
 gtctggatac agcgatgtga ctgacagcaa ggcaatgggg cccttggtg tgggctgcct 600
 caccaagtgc agccacgcct tccacctgct gtgcctcctg gccatgtact gcaacggcaa 660
 taagggccct gagcacccca atcccggaaa gccgttccact gccagagggt ttcccgccag 720
 tgctaccttc cagacaacgc cagggccgca agcctccagg ggcttccaga acccgagac 780
 actggctgac attccggcct cccacagct gctgaccgat ggccactaca tgacgctgcc 840
 cgtgtctccg gaccagctgc cctgtgacga ccccatggcg ggacgaggag gcgccccgt 900
 gctgcgggtg ggccatgacc acggctgcca ccagcagcca cgtatctgca acgcgccct 960
 ccctggccct ggaccctatc gtacagaacc tgctaaggcc atcaaaccta ttgatcgga 1020
 gtcagtccat cagatttgct ctgggccagt ggtactgagt ctaagcactg cagtgaagga 1080
 gttagtagaa aacagtctgg atgctggtgc cactaatatt gatctaaagc ttaaggacta 1140
 tggaatggat ctattgaag ttccaggcaa tggatgtggg gtagaagaag aaaacttcga 1200
 aggcttaatg atgtcaccat ttctacctgc cacgtctcgg cgaaggttgg gactcgactg 1260
 gtgtttgatc acgatgggaa aatcatccag aagacccctt acccccacc cagagggacc 1320
 acagtcagcg tgaagcagtt attttctacg ctacctgtgc gccataagga atttcaaagg 1380
 aatattaaga agaaacatgc tgcttcccct tcgccttctg ccgtgattgt cagttttaac 1440
 cgga 1445

<210> 26

<211> 270

<212> PRT

<213> Homo sapiens

<400> 26

Met Glu Lys Leu Ser Ala Ala Ser Gly Tyr Ser Asp Val Thr Asp Ser
 1 5 10 15

Lys Ala Met Gly Pro Leu Ala Val Gly Cys Leu Thr Lys Cys Ser His
 20 25 30

Ala Phe His Leu Leu Cys Leu Leu Ala Met Tyr Cys Asn Gly Asn Lys
 35 40 45

Gly Pro Glu His Pro Asn Pro Gly Lys Pro Phe Thr Ala Arg Gly Phe
 50 55 60

Pro Ala Ser Ala Thr Phe Gln Thr Thr Pro Gly Pro Gln Ala Ser Arg
 65 70 75 80

Gly Phe Gln Asn Pro Glu Thr Leu Ala Asp Ile Pro Ala Ser Pro Gln
 85 90 95

Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Val Ser Pro Asp Gln
 100 105 110

Leu Pro Cys Asp Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val Leu
 115 120 125

Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Arg Ile Cys Asn
 130 135 140

Ala Pro Leu Pro Gly Pro Gly Pro Tyr Arg Thr Glu Pro Ala Lys Ala
 145 150 155 160

Ile Lys Pro Ile Asp Arg Lys Ser Val His Gln Ile Cys Ser Gly Pro
 165 170 175

Val Val Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Val Glu Asn Ser
 180 185 190

Leu Asp Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly
 195 200 205

Met Asp Leu Ile Glu Val Ser Gly Asn Gly Cys Gly Val Glu Glu Glu
 210 215 220

Asn Phe Glu Gly Leu Met Met Ser Pro Phe Leu Pro Ala Thr Ser Arg
 225 230 235 240

Arg Arg Leu Gly Leu Asp Trp Cys Leu Ile Thr Met Gly Lys Ser Ser
 245 250 255

Arg Arg Pro Pro Thr Pro Thr Pro Glu Gly Pro Gln Ser Ala
 260 265 270

<210> 27
 <211> 795
 <212> DNA
 <213> Homo sapiens

<400> 27
 atgtgtcctt ggcggcctag actaggccgt cgctgtatgg tgagccccag ggaggcggat 60
 ctggggcccc agaaggacac ccgcctggat ttgccccgta gcccggcccc ggcccctcgg 120
 gaggagaaca gccttggtga ggtggacagg aggggacctc gcgagcagac gcgcgcgcca 180
 gcgacagcag ccccgccccg gcctctcggg agccgggggg cagaggctgc ggagccccag 240
 gaggtctat cagccacagt ctctgcatgt ttccaagagc aacaggaaat gaacacattg 300
 cagggggccag tgtcattcaa agatgtggct gtggatttca cccaggagga gtggcggcaa 360
 ctggaccctg atgagaagat agcatacggg gatgtgatgt tggagaacta cagccatcta 420
 gtttctgtgg ggtatgatta tcaccaagcc aaacatcatc atggagtga ggtgaaggaa 480
 gtggagcagg gagaggagcc gtggataatg gaaggtgaat ttccatgtca acatagtcca 540
 gaacctgcta aggccatcaa acctattgat cggaagtcag tccatcagat ttgctctggg 600
 ccagtggtag tgagtctaag cactgcagtg aaggagttag tagaaaacag tctggatgct 660
 ggtgccacta atattgatct aaagcttaag gactatggag tggatctcat tgaagtttca 720
 gacaatggat gtggggtaga agaagaaaac tttgaaggct taatctcttt cagctctgaa 780
 acatcacaca tgtaa 795

<210> 28
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 28

Met Cys Pro Trp Arg Pro Arg Leu Gly Arg Arg Cys Met Val Ser Pro
 1 5 10 15

Arg Glu Ala Asp Leu Gly Pro Gln Lys Asp Thr Arg Leu Asp Leu Pro
 20 25 30

Arg Ser Pro Ala Arg Ala Pro Arg Glu Gln Asn Ser Leu Gly Glu Val
 35 40 45

Asp Arg Arg Gly Pro Arg Glu Gln Thr Arg Ala Pro Ala Thr Ala Ala
 50 55 60

Pro Pro Arg Pro Leu Gly Ser Arg Gly Ala Glu Ala Ala Glu Pro Gln
 65 70 75 80

Glu Gly Leu Ser Ala Thr Val Ser Ala Cys Phe Gln Glu Gln Gln Glu
 85 90 95

MOR0251.ST25.txt

Met Asn Thr Leu Gln Gly Pro Val Ser Phe Lys Asp Val Ala Val Asp
 100 105 110

Phe Thr Gln Glu Glu Trp Arg Gln Leu Asp Pro Asp Glu Lys Ile Ala
 115 120 125

Tyr Gly Asp Val Met Leu Glu Asn Tyr Ser His Leu Val Ser Val Gly
 130 135 140

Tyr Asp Tyr His Gln Ala Lys His His His Gly Val Glu Val Lys Glu
 145 150 155 160

Val Glu Gln Gly Glu Glu Pro Trp Ile Met Glu Gly Glu Phe Pro Cys
 165 170 175

Gln His Ser Pro Glu Pro Ala Lys Ala Ile Lys Pro Ile Asp Arg Lys
 180 185 190

Ser Val His Gln Ile Cys Ser Gly Pro Val Val Leu Ser Leu Ser Thr
 195 200 205

Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp Ala Gly Ala Thr Asn
 210 215 220

Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp Leu Ile Glu Val Ser
 225 230 235 240

Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe Glu Gly Leu Ile Ser
 245 250 255

Phe Ser Ser Glu
 260

<210> 29
 <211> 3218
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 29
 aaataggaat gtgatacctt ctattgcatg caaagatagt gtaggaggcg ctgctattgc 60
 caaagacttt tgagaccgct tgctgtttca ttatagttga ggagttctcg aagacgagaa 120
 attagcagtt ttcggtgttt agtaatcgcg ctagcatgct aggacaattt aactgcaaaa 180
 ttttgatacg atagtgatag taaatggaag gtaaaaataa catagaccta tcaataagca 240
 atgtctctca gaataaaagc acttgatgca tcagtggtta acaaaattgc tgcaggtgag 300
 atcataatat cccccgtaaa tgctctcaaa gaaatgatgg agaattccat cgatgcgaat 360
 gctacaatga ttgatattct agtcaaggaa ggaggaatta aggtacttca aataacagat 420
 aacggatctg gaattaataa agcagacctg ccaatcttat gtgagcgatt cacgacgtcc 480
 aaattacaaa aattcgaaga tttgagtcag attcaaacgt atggattccg aggagaagct 540
 ttagccagta tctcacatgt ggcaagagtc acagtaacga caaaagttaa agaagacaga 600

MOR0251.ST25.txt

tgtgcatgga	gagtttcata	tgacagaaggt	aagatgttgg	aaagccccaa	acctgttgct	660
ggaaaagacg	gtaccacgat	cctagttgaa	gacctttttt	tcaatattcc	ttctagatta	720
agggccttga	ggtcccataa	tgatgaatac	tctaaaatat	tagatgttgt	cgggcgatac	780
gccattcatt	ccaaggacat	tggtttttct	tgtaaaaagt	tcggagactc	taattattct	840
ttatcagtta	aaccttcata	tacagtccag	gataggatta	ggactgtggt	caataaatct	900
gtggcttcga	atttaattac	ttttcatatc	agcaaagtag	aagattttaa	cctggaaagc	960
gttgatggaa	aggtgtgtaa	tttgaatttc	atatccaaaa	agtccatttc	attaattttt	1020
ttcattaata	atagactagt	gacatgtgat	cttctaagaa	gagctttgaa	cagcgtttac	1080
tccaattatc	tgccaaaggg	cttcagacct	tttattttat	tggaatttgt	tatagatccg	1140
gcggctgttg	atgttaacgt	tcacccgaca	aagagagagg	ttcgtttcct	gagccaagat	1200
gagatcatag	agaaaatcgc	caatcaattg	cacgccgaat	tatctgccat	tgatacttca	1260
cgtactttca	aggcttcttc	aatttcaaca	aacaagccag	agtcattgat	accattttaat	1320
gacaccatag	aaagtgatag	gaataggaag	agtctccgac	aagcccaagt	ggtagagaat	1380
tcatatacga	cagccaatag	tcaactaagg	aaagcgaaaa	gacaagagaa	taaactagtc	1440
agaatagatg	cttcacaagc	taaaattacg	tcatTTTTAT	cctcaagtca	acagttcaac	1500
tttgaaggat	cgtctacaaa	gcgacaactg	agtgaacca	aggtaacaaa	tgtaagccac	1560
tcccaagagg	cagaaaagct	gacactaaat	gaaagcgaac	aaccgcgtga	tgccaataca	1620
atcaatgata	atgacttgaa	ggatcaacct	aagaagaaac	aaaagttggg	ggattataaa	1680
gttccaagca	ttgccgatga	cgaaaagaat	gcactcccga	tttcaaaaga	cgggtatatt	1740
agagtaccta	aggagcgagt	taatgttaat	cttacgagta	tcaagaaatt	gcgtgaaaaa	1800
gtagatgatt	cgatacatcg	agaactaaca	gacatttttg	caaatttgaa	ttacgttggg	1860
gttgtagatg	aggaaagaag	attagccgct	attcagcatg	acttaaagct	ttttttaata	1920
gattacggat	ctgtgtgcta	tgagctattc	tatcagattg	gtttgacaga	cttcgcaaac	1980
tttggttaaga	taaacctaca	gagtacaaat	gtgtcagatg	atatagtttt	gtataatctc	2040
ctatcagaat	ttgacgagtt	aaatgacgat	gcttccaaag	aaaaaataat	tagtaaaata	2100
tgggacatga	gcagtatgct	aaatgagtac	tattccatag	aattggtgaa	tgatggtcta	2160
gataatgact	taaagtctgt	gaagctaaaa	tctctaccac	tactttttaa	aggctacatt	2220
ccatctctgg	tcaagttacc	atTTTTTATA	tatcgccctg	gtaaagaagt	tgattgggag	2280
gatgaacaag	agtgtctaga	tggtattttt	agagagattg	cattactcta	tatacctgat	2340
atggttccga	aagtcgatac	actcgatgca	tcgttgtcag	aagacgaaaa	agcccagttt	2400
ataaatagaa	aggaacacat	atcctcatta	ctagaacacg	ttctcttccc	ttgtatcaaa	2460
cgaaggttcc	tggtccctag	acacattctc	aaggatgtcg	tggaatagc	caaccttcca	2520
gatctataca	aagtTTTTTGA	gagggtgttaa	ctttaaaacg	ttttggctgt	aataccaaag	2580
TTTTTgttta	tttcttgagt	gtgattgtgt	ttcatttgaa	agtgtatgcc	ctttccttta	2640
acgattcatc	cgcgagattt	caaaggatat	gaaatatggg	tgagtttagg	aaagtatgtc	2700

MOR0251.ST25.txt

```

agaaatgtat attcggattg aaactcttct aatagttctg aagtcacttg gttccgtatt 2760
gttttcgtcc tcttcctcaa gcaacgattc ttgtctaagc ttattcaacg gtaccaaaga 2820
cccgagtcct tttatgagag aaaacatttc atcatttttc aactcaatta tcttaatatc 2880
attttgtagt attttgaaaa caggatggta aaacgaatca cctgaatcta gaagctgtac 2940
cttgtcccat aaaagtttta atttactgag cctttcggtc aagtaaaacta gtttatctag 3000
ttttgaaccg aatattgtgg gcagatttgc agtaagtcca gtttagatcta ctaaaagttg 3060
tttgacagca gccgattcca caaaaatttg gtaaaaggag atgaaagaga cctcgcgcgt 3120
aatggtttgc atcaccatcg gatgtctgtt gaaaaactca ctttttgcac ggaagttatt 3180
aacaataaga ctaatgatta ccttagaata atgtataa 3218

```

```

<210> 30
<211> 769
<212> PRT
<213> Saccharomyces cerevisiae
<400> 30

```

```

Met Ser Leu Arg Ile Lys Ala Leu Asp Ala Ser Val Val Asn Lys Ile
1          5          10          15

```

```

Ala Ala Gly Glu Ile Ile Ile Ser Pro Val Asn Ala Leu Lys Glu Met
          20          25          30

```

```

Met Glu Asn Ser Ile Asp Ala Asn Ala Thr Met Ile Asp Ile Leu Val
          35          40          45

```

```

Lys Glu Gly Gly Ile Lys Val Leu Gln Ile Thr Asp Asn Gly Ser Gly
          50          55          60

```

```

Ile Asn Lys Ala Asp Leu Pro Ile Leu Cys Glu Arg Phe Thr Thr Ser
65          70          75          80

```

```

Lys Leu Gln Lys Phe Glu Asp Leu Ser Gln Ile Gln Thr Tyr Gly Phe
          85          90          95

```

```

Arg Gly Glu Ala Leu Ala Ser Ile Ser His Val Ala Arg Val Thr Val
          100          105          110

```

```

Thr Thr Lys Val Lys Glu Asp Arg Cys Ala Trp Arg Val Ser Tyr Ala
          115          120          125

```

```

Glu Gly Lys Met Leu Glu Ser Pro Lys Pro Val Ala Gly Lys Asp Gly
          130          135          140

```

```

Thr Thr Ile Leu Val Glu Asp Leu Phe Phe Asn Ile Pro Ser Arg Leu
145          150          155          160

```

```

Arg Ala Leu Arg Ser His Asn Asp Glu Tyr Ser Lys Ile Leu Asp Val
          165          170          175

```

MOR0251.ST25.txt

Val Gly Arg Tyr Ala Ile His Ser Lys Asp Ile Gly Phe Ser Cys Lys
 180 185 190

Lys Phe Gly Asp Ser Asn Tyr Ser Leu Ser Val Lys Pro Ser Tyr Thr
 195 200 205

Val Gln Asp Arg Ile Arg Thr Val Phe Asn Lys Ser Val Ala Ser Asn
 210 215 220

Leu Ile Thr Phe His Ile Ser Lys Val Glu Asp Leu Asn Leu Glu Ser
 225 230 235 240

Val Asp Gly Lys Val Cys Asn Leu Asn Phe Ile Ser Lys Lys Ser Ile
 245 250 255

Ser Leu Ile Phe Phe Ile Asn Asn Arg Leu Val Thr Cys Asp Leu Leu
 260 265 270

Arg Arg Ala Leu Asn Ser Val Tyr Ser Asn Tyr Leu Pro Lys Gly Phe
 275 280 285

Arg Pro Phe Ile Tyr Leu Gly Ile Val Ile Asp Pro Ala Ala Val Asp
 290 295 300

Val Asn Val His Pro Thr Lys Arg Glu Val Arg Phe Leu Ser Gln Asp
 305 310 315 320

Glu Ile Ile Glu Lys Ile Ala Asn Gln Leu His Ala Glu Leu Ser Ala
 325 330 335

Ile Asp Thr Ser Arg Thr Phe Lys Ala Ser Ser Ile Ser Thr Asn Lys
 340 345 350

Pro Glu Ser Leu Ile Pro Phe Asn Asp Thr Ile Glu Ser Asp Arg Asn
 355 360 365

Arg Lys Ser Leu Arg Gln Ala Gln Val Val Glu Asn Ser Tyr Thr Thr
 370 375 380

Ala Asn Ser Gln Leu Arg Lys Ala Lys Arg Gln Glu Asn Lys Leu Val
 385 390 395 400

Arg Ile Asp Ala Ser Gln Ala Lys Ile Thr Ser Phe Leu Ser Ser Ser
 405 410 415

Gln Gln Phe Asn Phe Glu Gly Ser Ser Thr Lys Arg Gln Leu Ser Glu
 420 425 430

Pro Lys Val Thr Asn Val Ser His Ser Gln Glu Ala Glu Lys Leu Thr
 435 440 445

Leu Asn Glu Ser Glu Gln Pro Arg Asp Ala Asn Thr Ile Asn Asp Asn
 450 455 460

Asp Leu Lys Asp Gln Pro Lys Lys Lys Gln Lys Leu Gly Asp Tyr Lys
 465 470 475 480
 Val Pro Ser Ile Ala Asp Asp Glu Lys Asn Ala Leu Pro Ile Ser Lys
 485 490 495
 Asp Gly Tyr Ile Arg Val Pro Lys Glu Arg Val Asn Val Asn Leu Thr
 500 505 510
 Ser Ile Lys Lys Leu Arg Glu Lys Val Asp Asp Ser Ile His Arg Glu
 515 520 525
 Leu Thr Asp Ile Phe Ala Asn Leu Asn Tyr Val Gly Val Val Asp Glu
 530 535 540
 Glu Arg Arg Leu Ala Ala Ile Gln His Asp Leu Lys Leu Phe Leu Ile
 545 550 555 560
 Asp Tyr Gly Ser Val Cys Tyr Glu Leu Phe Tyr Gln Ile Gly Leu Thr
 565 570 575
 Asp Phe Ala Asn Phe Gly Lys Ile Asn Leu Gln Ser Thr Asn Val Ser
 580 585 590
 Asp Asp Ile Val Leu Tyr Asn Leu Leu Ser Glu Phe Asp Glu Leu Asn
 595 600 605
 Asp Asp Ala Ser Lys Glu Lys Ile Ile Ser Lys Ile Trp Asp Met Ser
 610 615 620
 Ser Met Leu Asn Glu Tyr Tyr Ser Ile Glu Leu Val Asn Asp Gly Leu
 625 630 635 640
 Asp Asn Asp Leu Lys Ser Val Lys Leu Lys Ser Leu Pro Leu Leu Leu
 645 650 655
 Lys Gly Tyr Ile Pro Ser Leu Val Lys Leu Pro Phe Phe Ile Tyr Arg
 660 665 670
 Leu Gly Lys Glu Val Asp Trp Glu Asp Glu Gln Glu Cys Leu Asp Gly
 675 680 685
 Ile Leu Arg Glu Ile Ala Leu Leu Tyr Ile Pro Asp Met Val Pro Lys
 690 695 700
 Val Asp Thr Leu Asp Ala Ser Leu Ser Glu Asp Glu Lys Ala Gln Phe
 705 710 715 720
 Ile Asn Arg Lys Glu His Ile Ser Ser Leu Leu Glu His Val Leu Phe
 725 730 735

Pro Cys Ile Lys Arg Arg Phe Leu Ala Pro Arg His Ile Leu Lys Asp
 740 745 750

Val Val Glu Ile Ala Asn Leu Pro Asp Leu Tyr Lys Val Phe Glu Arg
 755 760 765

Cys

<210> 31
 <211> 3056
 <212> DNA
 <213> Mus musculus

<400> 31
 gaattccggt gaaggtcctg aagaatttcc agattcctga gtatcattgg aggagacaga 60
 taacctgtcg tcaggtaacg atggtgtata tgcaacagaa atgggtgttc ctggagacgc 120
 gtcttttccc gagagcggca ccgcaactct cccgcggtga ctgtgactgg aggagtcctg 180
 catccatgga gcaaaccgaa ggcgtgagta cagaatgtgc taaggccatc aagcctattg 240
 atgggaagtc agtccatcaa atttgttctg ggcagggtgat actcagttta agcaccgctg 300
 tgaaggagtt gatagaaaat agtgtagatg ctgggtgctac tactattgat ctaaggctta 360
 aagactatgg ggtggacctc attgaagttt cagacaatgg atgtggggta gaagaagaaa 420
 actttgaagg tctagctctg aaacatcaca catctaagat tcaagagttt gccgacctca 480
 cgcagggtga aactttcggc ttctgggggg aagctctgag ctctctgtgt gactaagtg 540
 atgtcactat atctacctgc cacgggtctg caagcggttg gactcgactg gtgtttgacc 600
 ataatgggaa aatcacccag aaaactccct acccccgacc taaaggaacc acagtcaagt 660
 tgcagcactt attttataca ctaccctgac gttacaaaga gtttcagagg aacattaaaa 720
 aggagtattc caaaatggtg caggtcttac aggcgtactg tatcatctca gcaggcgtcc 780
 gtgtaagctg cactaatcag ctccggacag ggaagcggca cgctgtggtg tgcacaagcg 840
 gcacgtctgg catgaaggaa aatatcgggt ctgtgttttg ccagaagcag ttgcaaagcc 900
 tcattccttt tgttcagctg cccctagtg acgctgtgtg tgaagagtac ggcctgagca 960
 cttcaggacg ccacaaaacc ttttctacgt ttccggcttc atttcacagt gcacgcacgg 1020
 cgccgggagg agtgcaacag acaggcagtt tttcttcac aatcagaggc cctgtgaccc 1080
 agcaaaggtc tctaagcttg tcaatgaggt tttatcacat gtataaccgg catcagtacc 1140
 catttgcgt ccttaacggt tccgttgact cagaatgtgt ggatattaat gtaactccag 1200
 ataaaaggca aattctacta caagaagaga agctattgct ggccgtttta aagacctcct 1260
 tgataggaat gtttgacagt gatgcaaaca agcttaatgt caaccagcag cactgtctag 1320
 atgttgaagg taacttagta aagctgcata ctgcagaact agaaaagcct gtgccaggaa 1380
 agcaagataa ctctccttca ctgaagagca cagcagacga gaaaagggtg gcatccatct 1440
 ccaggctgag agaggccttt tctcttcac ctactaaaga gatcaagtct aggggtccag 1500
 agactgctga actgacacgg agttttccaa gtgagaaaaag ggcgtgttta tcctcttata 1560

MOR0251.ST25.txt

cttcagacgt catctcttac agaggcctcc gtggctcgca ggacaaattg gtgagtccca 1620
 cggacagccc tgggtgactgt atggacagag agaaaataga aaaagactca gggctcagca 1680
 gcacctcagc tggctctgag gaagagttca gcaccccaga agtggccagt agcttttagca 1740
 gtgactataa cgtgagctcc ctagaagaca gaccttctca ggaaccata aactgtggtg 1800
 acctggactg ccgctctcca ggtacaggac agtccttgaa gccagaagac catggatatac 1860
 aatgcaaagc tctacctcta gctcgtctgt caccacaaa tgccaagcgc ttcaagacag 1920
 aggaaagacc ctcaaagtgc aacatttctc aaagattgcc tggctcctcag agcacctcag 1980
 cagctgaggt cgatgtagcc ataaaaatga ataagagaat cgtgctcctc gagttctctc 2040
 tgagttctct agctaagcga atgaagcagt tacagcacct aaaggcgcag aacaaacatg 2100
 aactgagtta cagaaaattt agggccaaga tttgccctgg agaaaaccaa gcagcagaag 2160
 atgaactcag aaaagagatt agtaaactga tgtttgacaga gatggagatc ttgggtcagt 2220
 ttaacctggg atttatagta accaaactga aagaggacct ctctctgggtg gaccagcatg 2280
 ctgcggatga gaagtacaac tttgagatgc tgcagcagca cacggtgctc caggcgcaga 2340
 ggctcatcac accccagact ctgaacttaa ctgctgtcaa tgaagctgta ctgatagaaa 2400
 atctggaaat attcagaaag aatggctttg actttgtcat tgatgaggat gctccagtca 2460
 ctgaaagggc taaattgatt tccttaccaa ctagtaaaaa ctggaccttt ggacccaag 2520
 atatagatga actgatcttt atgttaagtg acagccctgg ggtcatgtgc cggccctcac 2580
 gagtcagaca gatgtttgct tccagagcct gtcggaagtc agtgatgatt ggaacggcgc 2640
 tcaatgcgag cgagatgaag aagctcatca cccacatggg tgagatggac caccctgga 2700
 actgccccca cggcaggcca accatgaggc acgttgccaa tctggatgtc atctctcaga 2760
 actgacacac cccttgtagc atagagttta ttacagattg ttcggtttgc aaagagaagg 2820
 ttttaagtaa tctgattatc gttgtacaaa aattagcatg ctgctttaat gtactggatc 2880
 catttaaaag cagtgttaag gcaggcatga tggagtgttc ctctagctca gctacttggg 2940
 tgatccggtg ggagctcatg tgagcccagg actttgagac cactccgagc cacattcatg 3000
 agactcaatt caaggacaaa aaaaaaaga tatttttgaa gccttttaaa aaaaaa 3056

<210> 32
 <211> 859
 <212> PRT
 <213> Mus musculus

<400> 32

Met Glu Gln Thr Glu Gly Val Ser Thr Glu Cys Ala Lys Ala Ile Lys
 1 5 10 15

Pro Ile Asp Gly Lys Ser Val His Gln Ile Cys Ser Gly Gln Val Ile
 20 25 30

Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Ile Glu Asn Ser Val Asp
 35 40 45

MOR0251.ST25.txt

Ala Gly Ala Thr Thr Ile Asp Leu Arg Leu Lys Asp Tyr Gly Val Asp
 50 55 60

Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe
 65 70 75 80

Glu Gly Leu Ala Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala
 85 90 95

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser
 100 105 110

Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Gly Ser
 115 120 125

Ala Ser Val Gly Thr Arg Leu Val Phe Asp His Asn Gly Lys Ile Thr
 130 135 140

Gln Lys Thr Pro Tyr Pro Arg Pro Lys Gly Thr Thr Val Ser Val Gln
 145 150 155 160

His Leu Phe Tyr Thr Leu Pro Val Arg Tyr Lys Glu Phe Gln Arg Asn
 165 170 175

Ile Lys Lys Glu Tyr Ser Lys Met Val Gln Val Leu Gln Ala Tyr Cys
 180 185 190

Ile Ile Ser Ala Gly Val Arg Val Ser Cys Thr Asn Gln Leu Gly Gln
 195 200 205

Gly Lys Arg His Ala Val Val Cys Thr Ser Gly Thr Ser Gly Met Lys
 210 215 220

Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile
 225 230 235 240

Pro Phe Val Gln Leu Pro Pro Ser Asp Ala Val Cys Glu Glu Tyr Gly
 245 250 255

Leu Ser Thr Ser Gly Arg His Lys Thr Phe Ser Thr Phe Arg Ala Ser
 260 265 270

Phe His Ser Ala Arg Thr Ala Pro Gly Gly Val Gln Gln Thr Gly Ser
 275 280 285

Phe Ser Ser Ser Ile Arg Gly Pro Val Thr Gln Gln Arg Ser Leu Ser
 290 295 300

Leu Ser Met Arg Phe Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe
 305 310 315 320

Val Val Leu Asn Val Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val
 325 330 335

Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu
 340 345 350
 Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Ala Asn
 355 360 365
 Lys Leu Asn Val Asn Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu
 370 375 380
 Val Lys Leu His Thr Ala Glu Leu Glu Lys Pro Val Pro Gly Lys Gln
 385 390 395 400
 Asp Asn Ser Pro Ser Leu Lys Ser Thr Ala Asp Glu Lys Arg Val Ala
 405 410 415
 Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu His Pro Thr Lys Glu
 420 425 430
 Ile Lys Ser Arg Gly Pro Glu Thr Ala Glu Leu Thr Arg Ser Phe Pro
 435 440 445
 Ser Glu Lys Arg Gly Val Leu Ser Ser Tyr Pro Ser Asp Val Ile Ser
 450 455 460
 Tyr Arg Gly Leu Arg Gly Ser Gln Asp Lys Leu Val Ser Pro Thr Asp
 465 470 475 480
 Ser Pro Gly Asp Cys Met Asp Arg Glu Lys Ile Glu Lys Asp Ser Gly
 485 490 495
 Leu Ser Ser Thr Ser Ala Gly Ser Glu Glu Glu Phe Ser Thr Pro Glu
 500 505 510
 Val Ala Ser Ser Phe Ser Ser Asp Tyr Asn Val Ser Ser Leu Glu Asp
 515 520 525
 Arg Pro Ser Gln Glu Thr Ile Asn Cys Gly Asp Leu Asp Cys Arg Pro
 530 535 540
 Pro Gly Thr Gly Gln Ser Leu Lys Pro Glu Asp His Gly Tyr Gln Cys
 545 550 555 560
 Lys Ala Leu Pro Leu Ala Arg Leu Ser Pro Thr Asn Ala Lys Arg Phe
 565 570 575
 Lys Thr Glu Glu Arg Pro Ser Asn Val Asn Ile Ser Gln Arg Leu Pro
 580 585 590
 Gly Pro Gln Ser Thr Ser Ala Ala Glu Val Asp Val Ala Ile Lys Met
 595 600 605

MOR0251.ST25.txt

Asn Lys Arg Ile Val Leu Leu Glu Phe Ser Leu Ser Ser Leu Ala Lys
 610 615 620
 Arg Met Lys Gln Leu Gln His Leu Lys Ala Gln Asn Lys His Glu Leu
 625 630 635 640
 Ser Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala
 645 650 655
 Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Ser Met Phe Ala Glu
 660 665 670
 Met Glu Ile Leu Gly Gln Phe Asn Leu Gly Phe Ile Val Thr Lys Leu
 675 680 685
 Lys Glu Asp Leu Phe Leu Val Asp Gln His Ala Ala Asp Glu Lys Tyr
 690 695 700
 Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Ala Gln Arg Leu
 705 710 715 720
 Ile Thr Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu Ala Val Leu
 725 730 735
 Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp Phe Val Ile
 740 745 750
 Asp Glu Asp Ala Pro Val Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro
 755 760 765
 Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Ile Asp Glu Leu Ile
 770 775 780
 Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro Ser Arg Val
 785 790 795 800
 Arg Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val Met Ile Gly
 805 810 815
 Thr Ala Leu Asn Ala Ser Glu Met Lys Lys Leu Ile Thr His Met Gly
 820 825 830
 Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro Thr Met Arg
 835 840 845
 His Val Ala Asn Leu Asp Val Ile Ser Gln Asn
 850 855

<210> 33
 <211> 399
 <212> DNA
 <213> Mus musculus
 <400> 33

MOR0251.ST25.txt

```

atggagcaaa ccgaaggcgt gactacagaa tgtgctaagg ccatcaagcc tattgatggg      60
aagtcagtcc atcaaatttg ttctgggcag gtgatactca gtttaagcac cgctgtgaag      120
gagttgatag aaaatagtgt agatgctggt gctactacta ttgatctaag gcttaaagac      180
tatggggtgg acctcattga agtttcagac aatggatgtg gggtagaaga agaaaacttt      240
gaaggtctag ctctgaaaca tcacacatct aagattcaag agtttgccga cctcacgcag      300
gttgaaactt tcggctttcg gggggaagct ctgagctctc tgtgtgcact aagtgatgtc      360
actatatcta cctgccacgg gtctgcaagc gttgggact                                399

```

```

<210> 34
<211> 133
<212> PRT
<213> Mus musculus

```

```

<400> 34

```

```

Met Glu Gln Thr Glu Gly Val Ser Thr Glu Cys Ala Lys Ala Ile Lys
1          5          10          15

```

```

Pro Ile Asp Gly Lys Ser Val His Gln Ile Cys Ser Gly Gln Val Ile
          20          25          30

```

```

Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Ile Glu Asn Ser Val Asp
          35          40          45

```

```

Ala Gly Ala Thr Thr Ile Asp Leu Arg Leu Lys Asp Tyr Gly Val Asp
          50          55          60

```

```

Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe
65          70          75          80

```

```

Glu Gly Leu Ala Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala
          85          90          95

```

```

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser
          100          105          110

```

```

Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Gly Ser
          115          120          125

```

```

Ala Ser Val Gly Thr
          130

```

```

<210> 35
<211> 3099
<212> DNA
<213> Arabidopsis thaliana

```

```

<400> 35
gtcttcttct tcatccttgt ctcaccttcg attttggcgg caaaacataa accctaaggg      60
ttttctcact ctctctctct cttctcacac acacagtcctc agagtacggt ggtgttgatt      120
cgattgagga gattcatctg tttatagggt ttagcaaatg caaggagatt cttctccgctc      180

```

MOR0251.ST25.txt

tccgacgact	actagctctc	ctttgataag	acctataaac	agaaacgtaa	ttcacagaat	240
ctgttccggt	caagtcatct	tagacctctc	ttcgcccgtc	aaggagcttg	tcgagaatag	300
tctcgacgcc	ggcgccacca	gtatagagat	taacctccga	gactacggcg	aagactattt	360
tcaggtcatt	gacaatgggt	gtggcatttc	cccaaccaat	ttcaaggttc	ttgcacttaa	420
gcatcatact	tctaaattag	aggatttcac	agatcttttg	aatttgacta	cttatggttt	480
tagaggagaa	gccttgagct	ctctctgtgc	attgggaaat	ctcactgtgg	aaacaagaac	540
aaagaatgag	ccagttgcta	cgctcttgac	gtttgatcat	tctggtttgc	ttactgctga	600
aaagaagact	gctcgccaaa	ttggtaccac	tgtcactgtt	aggaagttgt	tctctaattt	660
acctgtacga	agcaaagagt	ttaagcggaa	tatacgcaaa	gaatatggga	agcttgtatc	720
tttattgaac	gcatatgcgc	ttattgcgaa	aggagtgcgg	tttgtctgct	ctaacacgac	780
tgggaaaaac	ccaaagtctg	ttgtgctgaa	cacacaaggg	aggggttcac	ttaaagataa	840
tatcataaca	gttttcggca	ttagtacctt	tacaagtcta	cagcctgtaa	gtatatgtgt	900
atcagaagat	tgtagagttg	aagggtttct	ttccaagcct	ggacagggta	ctggacgcaa	960
tttagcagat	cgacagtatt	tctttataaa	tggtcggcct	gtagatatgc	caaaagtcag	1020
caagttggtg	aatgagttat	ataaagatac	aagttctcgg	aaatatccag	ttaccattct	1080
ggattttatt	gtgcctggtg	gagcatgtga	ttgaaatgtc	acgcccgata	aaagaaaggt	1140
gttcttttct	gacgagactt	ctgttatcgg	ttctttgagg	gaaggctctga	acgagatata	1200
ttcctccagt	aatgctgtct	atattgttaa	taggttcgag	gagaattcgg	agcaaccaga	1260
taaggctgga	gtttcgtcgt	ttcagaagaa	atcaaactct	ttgtcagaag	ggatagttct	1320
ggatgtcagt	tctaaaacaa	gactagggga	agctattgag	aaagaaaatc	catccttaag	1380
ggaggttgaa	attgataata	gttcgccaat	ggagaagttt	aagtttgaga	tcaaggcatg	1440
tgggacgaag	aaaggggaag	gttctttatc	agtccatgat	gtaactcacc	ttgacaagac	1500
acctagcaaa	ggtttgcctc	agttaaatgt	gactgagaaa	gttactgatg	caagtaaaga	1560
cttgagcagc	cgctctagct	ttgccagtc	aactttgaat	acttttgtaa	ccatgggaaa	1620
aagaaaacat	gaaaacataa	gcaccatcct	ctctgaaaca	cctgtcctca	gaaaccaaac	1680
ttctagttat	cgtgtggaga	aaagcaaatt	tgaagttcgt	gccttagctt	caaggtgtct	1740
cgtggaaggc	gatcaacttg	atgatatggt	catctcaaag	gaagatatga	caccaagcga	1800
aagagattct	gaactaggca	atcggatttc	tcttgaaca	caagctgata	atgttgaaag	1860
acatgagaga	gaacatgaaa	agcctataag	gtttgaagaa	ccaacatcag	ataacacact	1920
caccaagggg	gatgtggaaa	gggtttcaga	ggacaatcca	cggtgcagtc	agccactgcg	1980
atctgtggcc	acagtgtctg	attccccagc	tcagtcaacc	ggtcctaaaa	tgttttccac	2040
attagaatth	agtttccaaa	acctcaggac	aaggagggtta	gagaggctgt	cgagattgca	2100
gtccacaggt	tatgtatcta	aatgtatgaa	tacgccacag	cctaaaaagt	gctttgccgc	2160
tgcaacatta	gagttatctc	aaccggatga	tgaagagcga	aaagcaaggg	ctttagctgc	2220
agctacttct	gagctggaaa	ggcttttttcg	aaaagaggat	ttcaggagaa	tgcaggtact	2280

MOR0251.ST25.txt

cgggcaattc aatcttgggt tcatcattgc aaaattggag cgagatctgt tcattgtgga 2340
 tcagcatgca gctgatgaga aattcaactt cgaacattta gcaagggtcaa ctgtcctgaa 2400
 ccagcaaccc ttactccagc ctttgaactt ggaactctct ccagaagaag aagtaactgt 2460
 gttaatgcac atggatatta tcagggaaaa tggctttctt ctagaggaga atccaagtgc 2520
 tcctcccgga aaacacttta gactacgagc cattccttat agcaagaata tcacctttgg 2580
 agtcgaagat cttaaagacc tgatctcaac tctaggagat aaccatgggg aatgttcggt 2640
 tgctagtagc taaaaacca gaaaaacaga ttcgatttgt ccatcacgag tccgtgcaat 2700
 gctagcatcc cgagcatgca gatcatctgt gatgatcgga gatccactca gaaaaaacga 2760
 aatgcagaag atagtagaac acttggcaga tctcgaatct ccttgggaatt gcccacacgg 2820
 acgaccaaca atgcgtcatc ttgtggactt gacaacttta ctcacattac ctgatgacga 2880
 caatgtcaat gatgatgatg atgatgatgc aaccatctca ttggcatgaa cactcaaaag 2940
 tcttaacgta tttagatgtg agaatcctta agattaacat tgaggaacac tcggttataa 3000
 ctacaatcgt aaatgtaaat tgtcttagtc tatatgatct ttttggtcac aacaggtaat 3060
 ttcattttcc tttgattact tctcgtgaaa aaacaaatt 3099

<210> 36
 <211> 923
 <212> PRT
 <213> Arabidopsis thaliana

<400> 36

Met Gln Gly Asp Ser Ser Pro Ser Pro Thr Thr Thr Ser Ser Pro Leu
 1 5 10 15

Ile Arg Pro Ile Asn Arg Asn Val Ile His Arg Ile Cys Ser Gly Gln
 20 25 30

Val Ile Leu Asp Leu Ser Ser Ala Val Lys Glu Leu Val Glu Asn Ser
 35 40 45

Leu Asp Ala Gly Ala Thr Ser Ile Glu Ile Asn Leu Arg Asp Tyr Gly
 50 55 60

Glu Asp Tyr Phe Gln Val Ile Asp Asn Gly Cys Gly Ile Ser Pro Thr
 65 70 75 80

Asn Phe Lys Val Leu Ala Leu Lys His His Thr Ser Lys Leu Glu Asp
 85 90 95

Phe Thr Asp Leu Leu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala
 100 105 110

Leu Ser Ser Leu Cys Ala Leu Gly Asn Leu Thr Val Glu Thr Arg Thr
 115 120 125

Lys Asn Glu Pro Val Ala Thr Leu Leu Thr Phe Asp His Ser Gly Leu
 130 135 140

Leu Thr Ala Glu Lys Lys Thr Ala Arg Gln Ile Gly Thr Thr Val Thr
 145 150 155 160
 Val Arg Lys Leu Phe Ser Asn Leu Pro Val Arg Ser Lys Glu Phe Lys
 165 170 175
 Arg Asn Ile Arg Lys Glu Tyr Gly Lys Leu Val Ser Leu Leu Asn Ala
 180 185 190
 Tyr Ala Leu Ile Ala Lys Gly Val Arg Phe Val Cys Ser Asn Thr Thr
 195 200 205
 Gly Lys Asn Pro Lys Ser Val Val Leu Asn Thr Gln Gly Arg Gly Ser
 210 215 220
 Leu Lys Asp Asn Ile Ile Thr Val Phe Gly Ile Ser Thr Phe Thr Ser
 225 230 235 240
 Leu Gln Pro Val Ser Ile Cys Val Ser Glu Asp Cys Arg Val Glu Gly
 245 250 255
 Phe Leu Ser Lys Pro Gly Gln Gly Thr Gly Arg Asn Leu Ala Asp Arg
 260 265 270
 Gln Tyr Phe Phe Ile Asn Gly Arg Pro Val Asp Met Pro Lys Val Ser
 275 280 285
 Lys Leu Val Asn Glu Leu Tyr Lys Asp Thr Ser Ser Arg Lys Tyr Pro
 290 295 300
 Val Thr Ile Leu Asp Phe Ile Val Pro Gly Gly Ala Cys Asp Leu Asn
 305 310 315 320
 Val Thr Pro Asp Lys Arg Lys Val Phe Phe Ser Asp Glu Thr Ser Val
 325 330 335
 Ile Gly Ser Leu Arg Glu Gly Leu Asn Glu Ile Tyr Ser Ser Ser Asn
 340 345 350
 Ala Ser Tyr Ile Val Asn Arg Phe Glu Glu Asn Ser Glu Gln Pro Asp
 355 360 365
 Lys Ala Gly Val Ser Ser Phe Gln Lys Lys Ser Asn Leu Leu Ser Glu
 370 375 380
 Gly Ile Val Leu Asp Val Ser Ser Lys Thr Arg Leu Gly Glu Ala Ile
 385 390 395 400
 Glu Lys Glu Asn Pro Ser Leu Arg Glu Val Glu Ile Asp Asn Ser Ser
 405 410 415

MOR0251.ST25.txt

Pro Met Glu Lys Phe Lys Phe Glu Ile Lys Ala Cys Gly Thr Lys Lys
 420 425 430

Gly Glu Gly Ser Leu Ser Val His Asp Val Thr His Leu Asp Lys Thr
 435 440 445

Pro Ser Lys Gly Leu Pro Gln Leu Asn Val Thr Glu Lys Val Thr Asp
 450 455 460

Ala Ser Lys Asp Leu Ser Ser Arg Ser Ser Phe Ala Gln Ser Thr Leu
 465 470 475 480

Asn Thr Phe Val Thr Met Gly Lys Arg Lys His Glu Asn Ile Ser Thr
 485 490 495

Ile Leu Ser Glu Thr Pro Val Leu Arg Asn Gln Thr Ser Ser Tyr Arg
 500 505 510

Val Glu Lys Ser Lys Phe Glu Val Arg Ala Leu Ala Ser Arg Cys Leu
 515 520 525

Val Glu Gly Asp Gln Leu Asp Asp Met Val Ile Ser Lys Glu Asp Met
 530 535 540

Thr Pro Ser Glu Arg Asp Ser Glu Leu Gly Asn Arg Ile Ser Pro Gly
 545 550 555 560

Thr Gln Ala Asp Asn Val Glu Arg His Glu Arg Glu His Glu Lys Pro
 565 570 575

Ile Arg Phe Glu Glu Pro Thr Ser Asp Asn Thr Leu Thr Lys Gly Asp
 580 585 590

Val Glu Arg Val Ser Glu Asp Asn Pro Arg Cys Ser Gln Pro Leu Arg
 595 600 605

Ser Val Ala Thr Val Leu Asp Ser Pro Ala Gln Ser Thr Gly Pro Lys
 610 615 620

Met Phe Ser Thr Leu Glu Phe Ser Phe Gln Asn Leu Arg Thr Arg Arg
 625 630 635 640

Leu Glu Arg Leu Ser Arg Leu Gln Ser Thr Gly Tyr Val Ser Lys Cys
 645 650 655

Met Asn Thr Pro Gln Pro Lys Lys Cys Phe Ala Ala Ala Thr Leu Glu
 660 665 670

Leu Ser Gln Pro Asp Asp Glu Glu Arg Lys Ala Arg Ala Leu Ala Ala
 675 680 685

Ala Thr Ser Glu Leu Glu Arg Leu Phe Arg Lys Glu Asp Phe Arg Arg
 690 695 700

Met Gln Val Leu Gly Gln Phe Asn Leu Gly Phe Ile Ile Ala Lys Leu
705 710 715 720

Glu Arg Asp Leu Phe Ile Val Asp Gln His Ala Ala Asp Glu Lys Phe
725 730 735

Asn Phe Glu His Leu Ala Arg Ser Thr Val Leu Asn Gln Gln Pro Leu
740 745 750

Leu Gln Pro Leu Asn Leu Glu Leu Ser Pro Glu Glu Glu Val Thr Val
755 760 765

Leu Met His Met Asp Ile Ile Arg Glu Asn Gly Phe Leu Leu Glu Glu
770 775 780

Asn Pro Ser Ala Pro Pro Gly Lys His Phe Arg Leu Arg Ala Ile Pro
785 790 795 800

Tyr Ser Lys Asn Ile Thr Phe Gly Val Glu Asp Leu Lys Asp Leu Ile
805 810 815

Ser Thr Leu Gly Asp Asn His Gly Glu Cys Ser Val Ala Ser Ser Tyr
820 825 830

Lys Thr Ser Lys Thr Asp Ser Ile Cys Pro Ser Arg Val Arg Ala Met
835 840 845

Leu Ala Ser Arg Ala Cys Arg Ser Ser Val Met Ile Gly Asp Pro Leu
850 855 860

Arg Lys Asn Glu Met Gln Lys Ile Val Glu His Leu Ala Asp Leu Glu
865 870 875 880

Ser Pro Trp Asn Cys Pro His Gly Arg Pro Thr Met Arg His Leu Val
885 890 895

Asp Leu Thr Thr Leu Leu Thr Leu Pro Asp Asp Asp Asn Val Asn Asp
900 905 910

Asp Asp Asp Asp Asp Ala Thr Ile Ser Leu Ala
915 920

<210> 37
<211> 399
<212> DNA
<213> Arabidopsis thaliana

<400> 37
atgcaaggag attcttctcc gtctccgacg actactagct ctcctttgat aagacctata 60
aacagaaacg taattcacag aatctgttcc ggtcaagtca tcttagacct ctcttcggcc 120
gtcaaggagc ttgtcgagaa tagtctcgac gccggcgcca ccagtataga gattaacctc 180

MOR0251.ST25.txt

cgagactacg gcgaagacta ttttcaggtc attgacaatg gttgtggcat ttccccaacc 240
 aatttcaagg ttcttgcaact taagcatcat acttctaaat tagaggattt cacagatctt 300
 ttgaatttga ctacttatgg ttttagagga gaagccttga gctctctctg tgcattggga 360
 aatctcactg tggaacaag aacaaagaat gagccagtt 399

<210> 38
 <211> 133
 <212> PRT
 <213> Arabidopsis thaliana

<400> 38

Met Gln Gly Asp Ser Ser Pro Ser Pro Thr Thr Thr Ser Ser Pro Leu
 1 5 10 15

Ile Arg Pro Ile Asn Arg Asn Val Ile His Arg Ile Cys Ser Gly Gln
 20 25 30

Val Ile Leu Asp Leu Ser Ser Ala Val Lys Glu Leu Val Glu Asn Ser
 35 40 45

Leu Asp Ala Gly Ala Thr Ser Ile Glu Ile Asn Leu Arg Asp Tyr Gly
 50 55 60

Glu Asp Tyr Phe Gln Val Ile Asp Asn Gly Cys Gly Ile Ser Pro Thr
 65 70 75 80

Asn Phe Lys Val Leu Ala Leu Lys His His Thr Ser Lys Leu Glu Asp
 85 90 95

Phe Thr Asp Leu Leu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala
 100 105 110

Leu Ser Ser Leu Cys Ala Leu Gly Asn Leu Thr Val Glu Thr Arg Thr
 115 120 125

Lys Asn Glu Pro Val
 130

<210> 39
 <211> 2772
 <212> DNA
 <213> Arabidopsis thaliana

<400> 39

atgcaaggag attcttctcc gtctccgacg actactagct ctcttttgat aagacctata 60
 aacagaaaacg taattcacag aatctgttcc ggtcaagtca tcttagacct ctcttcggcc 120
 gtcaaggagc ttgtcgagaa tagtctcgac gccggcgcca ccagtataga gattaacctc 180
 cgagactacg gcgaagacta ttttcaggtc attgacaatg gttgtggcat ttccccaacc 240
 aatttcaagg ttcttgcaact taagcatcat acttctaaat tagaggattt cacagatctt 300
 ttgaatttga ctacttatgg ttttagagga gaagccttga gctctctctg tgcattggga 360

MOR0251.ST25.txt

aatctcactg	tggaacaag	aacaaagaat	gagccagttg	ctacgctctt	gacgtttgat	420
cattctggtt	tgcttactgc	tgaaaagaag	actgctcgcc	aaattggtac	cactgtcact	480
gttaggaagt	tgttctctaa	tttacctgta	cgaagcaaag	agtttaagcg	gaatatacgc	540
aaagaatatg	ggaagcttgt	atctttattg	aacgcataatg	cgcttattgc	gaaaggagtg	600
cggtttgtct	gctctaacac	gactgggaaa	aacccaaagt	ctgttgtgct	gaacacacaa	660
gggagggtt	cacttaaaga	taatatcata	acagttttcg	gcattagtag	ctttacaagt	720
ctacagcctg	taagtatatg	tgtatcagaa	gattgtagag	ttgaagggtt	tctttccaag	780
cctggacagg	gtactggacg	caatttagca	gatcgacagt	atctctttat	aaatggtcgg	840
cctgtagata	tgccaaaagt	cagcaagttg	gtgaatgagt	tatataaaga	tacaagttct	900
cggaaatata	cagttaccat	tctggatttt	attgtgcctg	gtggagcatg	tgatttgaat	960
gtcacgccc	ataaaagaaa	ggtgttcttt	tctgacgaga	cttctgttat	cgttctttt	1020
agggaaggtc	tgaacgagat	atattcctcc	agtaatgcgt	cttatattgt	taataggttc	1080
gaggagaatt	cggagcaacc	agataaggct	ggagtttctg	cgtttcagaa	gaaatcaaat	1140
cttttgtcag	aagggatagt	tctggatgtc	agttctaaaa	caagactagg	ggaagctatt	1200
gagaaagaaa	atccatcctt	aaggagggtt	gaaattgata	atagttcgcc	aatggagaag	1260
tttaagtttg	agatcaaggc	atgtgggacg	aagaaagggg	aaggttcttt	atcagtccat	1320
gatgtaactc	accttgacaa	gacacctagc	aaaggtttgc	ctcagttaaa	tgtgactgag	1380
aaagttactg	atgcaagtaa	agacttgagc	agccgctcta	gctttgccc	gtcaactttg	1440
aatacttttg	ttaccatggg	aaaaagaaaa	catgaaaaca	taagcaccat	cctctctgaa	1500
acacctgtcc	tcagaaacca	aacttctagt	tatcgtgtgg	agaaaagcaa	atttgaagtt	1560
cgtgccttag	cttcaagggt	tctcgtggaa	ggcgatcaac	ttgatgatat	ggatcatctca	1620
aaggaagata	tgacaccaag	cgaaagagat	tctgaactag	gcaatcggat	ttctcctgga	1680
acacaagctg	ataatgttga	aagacatgag	agagaacatg	aaaagcctat	aaggtttgaa	1740
gaaccaacat	cagataacac	actcaccaag	ggggatgtgg	aaagggtttc	agaggacaat	1800
ccacggtgca	gtcagccact	gcgatctgtg	gccacagtgc	tggtattccc	agctcagtca	1860
accggtccta	aaatgttttc	cacattagaa	tttagtttcc	aaaacctcag	gacaaggagg	1920
ttagagaggc	tgtcgagatt	gcagtccaca	ggttatgtat	ctaaatgtat	gaatacgcca	1980
cagcctaaaa	agtgtcttgc	cgctgcaaca	ttagagttat	ctcaaccgga	tgatgaagag	2040
cgaaaagcaa	gggcttttag	tgcagctact	tctgagctgg	aaaggctttt	tcgaaaagag	2100
gatttcagga	gaatgcaggt	actcgggcaa	ttcaatcttg	ggttcatcat	tgcaaaattg	2160
gagcgagatc	tgttcattgt	ggatcagcat	gcagctgatg	agaaattcaa	cttcgaacat	2220
ttagcaaggt	caactgtcct	gaaccagcaa	cccttactcc	agcctttgaa	cttggaactc	2280
tctccagaag	aagaagtaac	tgtgttaatg	cacatggata	ttatcagga	aaatggcttt	2340
cttctagagg	agaatccaag	tgctcctccc	ggaaaacact	ttagactacg	agccattcct	2400
tatagcaaga	atatcacctt	tggagtcgaa	gatcttaaa	acctgatctc	aactctagga	2460

MOR0251.ST25.txt

gataaccatg gggaatgttc ggttgctagt agctacaaaa ccagcaaaac agattcgatt 2520
 tgtccatcac gagtccgtgc aatgctagca tcccagcat gcagatcatc tgtgatgatc 2580
 ggagatccac tcagaaaaaa cgaaatgcag aagatagtag aacacttggc agatctcgaa 2640
 tctccttgga attgcccaca cggacgacca acaatgcgtc atcttggtga cttgacaact 2700
 ttactcacat tacctgatga cgacaatgtc aatgatgatg atgatgatga tgcaaccatc 2760
 tcattggcat ga 2772

<210> 40
 <211> 923
 <212> PRT
 <213> Arabidopsis thaliana

<400> 40

Met Gln Gly Asp Ser Ser Pro Ser Pro Thr Thr Thr Ser Ser Pro Leu
 1 5 10 15

Ile Arg Pro Ile Asn Arg Asn Val Ile His Arg Ile Cys Ser Gly Gln
 20 25 30

Val Ile Leu Asp Leu Ser Ser Ala Val Lys Glu Leu Val Glu Asn Ser
 35 40 45

Leu Asp Ala Gly Ala Thr Ser Ile Glu Ile Asn Leu Arg Asp Tyr Gly
 50 55 60

Glu Asp Tyr Phe Gln Val Ile Asp Asn Gly Cys Gly Ile Ser Pro Thr
 65 70 75 80

Asn Phe Lys Val Leu Ala Leu Lys His His Thr Ser Lys Leu Glu Asp
 85 90 95

Phe Thr Asp Leu Leu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala
 100 105 110

Leu Ser Ser Leu Cys Ala Leu Gly Asn Leu Thr Val Glu Thr Arg Thr
 115 120 125

Lys Asn Glu Pro Val Ala Thr Leu Leu Thr Phe Asp His Ser Gly Leu
 130 135 140

Leu Thr Ala Glu Lys Lys Thr Ala Arg Gln Ile Gly Thr Thr Val Thr
 145 150 155 160

Val Arg Lys Leu Phe Ser Asn Leu Pro Val Arg Ser Lys Glu Phe Lys
 165 170 175

Arg Asn Ile Arg Lys Glu Tyr Gly Lys Leu Val Ser Leu Leu Asn Ala
 180 185 190

Tyr Ala Leu Ile Ala Lys Gly Val Arg Phe Val Cys Ser Asn Thr Thr
 195 200 205

Gly Lys Asn Pro Lys Ser Val Val Leu Asn Thr Gln Gly Arg Gly Ser
 210 215 220
 Leu Lys Asp Asn Ile Ile Thr Val Phe Gly Ile Ser Thr Phe Thr Ser
 225 230 235 240
 Leu Gln Pro Val Ser Ile Cys Val Ser Glu Asp Cys Arg Val Glu Gly
 245 250 255
 Phe Leu Ser Lys Pro Gly Gln Gly Thr Gly Arg Asn Leu Ala Asp Arg
 260 265 270
 Gln Tyr Phe Phe Ile Asn Gly Arg Pro Val Asp Met Pro Lys Val Ser
 275 280 285
 Lys Leu Val Asn Glu Leu Tyr Lys Asp Thr Ser Ser Arg Lys Tyr Pro
 290 295 300
 Val Thr Ile Leu Asp Phe Ile Val Pro Gly Gly Ala Cys Asp Leu Asn
 305 310 315 320
 Val Thr Pro Asp Lys Arg Lys Val Phe Phe Ser Asp Glu Thr Ser Val
 325 330 335
 Ile Gly Ser Leu Arg Glu Gly Leu Asn Glu Ile Tyr Ser Ser Ser Asn
 340 345 350
 Ala Ser Tyr Ile Val Asn Arg Phe Glu Glu Asn Ser Glu Gln Pro Asp
 355 360 365
 Lys Ala Gly Val Ser Ser Phe Gln Lys Lys Ser Asn Leu Leu Ser Glu
 370 375 380
 Gly Ile Val Leu Asp Val Ser Ser Lys Thr Arg Leu Gly Glu Ala Ile
 385 390 395 400
 Glu Lys Glu Asn Pro Ser Leu Arg Glu Val Glu Ile Asp Asn Ser Ser
 405 410 415
 Pro Met Glu Lys Phe Lys Phe Glu Ile Lys Ala Cys Gly Thr Lys Lys
 420 425 430
 Gly Glu Gly Ser Leu Ser Val His Asp Val Thr His Leu Asp Lys Thr
 435 440 445
 Pro Ser Lys Gly Leu Pro Gln Leu Asn Val Thr Glu Lys Val Thr Asp
 450 455 460
 Ala Ser Lys Asp Leu Ser Ser Arg Ser Ser Phe Ala Gln Ser Thr Leu
 465 470 475 480

Asn Thr Phe Val Thr Met Gly Lys Arg Lys His Glu Asn Ile Ser Thr
 485 490 495

Ile Leu Ser Glu Thr Pro Val Leu Arg Asn Gln Thr Ser Ser Tyr Arg
 500 505 510

Val Glu Lys Ser Lys Phe Glu Val Arg Ala Leu Ala Ser Arg Cys Leu
 515 520 525

Val Glu Gly Asp Gln Leu Asp Asp Met Val Ile Ser Lys Glu Asp Met
 530 535 540

Thr Pro Ser Glu Arg Asp Ser Glu Leu Gly Asn Arg Ile Ser Pro Gly
 545 550 555 560

Thr Gln Ala Asp Asn Val Glu Arg His Glu Arg Glu His Glu Lys Pro
 565 570 575

Ile Arg Phe Glu Glu Pro Thr Ser Asp Asn Thr Leu Thr Lys Gly Asp
 580 585 590

Val Glu Arg Val Ser Glu Asp Asn Pro Arg Cys Ser Gln Pro Leu Arg
 595 600 605

Ser Val Ala Thr Val Leu Asp Ser Pro Ala Gln Ser Thr Gly Pro Lys
 610 615 620

Met Phe Ser Thr Leu Glu Phe Ser Phe Gln Asn Leu Arg Thr Arg Arg
 625 630 635 640

Leu Glu Arg Leu Ser Arg Leu Gln Ser Thr Gly Tyr Val Ser Lys Cys
 645 650 655

Met Asn Thr Pro Gln Pro Lys Lys Cys Phe Ala Ala Ala Thr Leu Glu
 660 665 670

Leu Ser Gln Pro Asp Asp Glu Glu Arg Lys Ala Arg Ala Leu Ala Ala
 675 680 685

Ala Thr Ser Glu Leu Glu Arg Leu Phe Arg Lys Glu Asp Phe Arg Arg
 690 695 700

Met Gln Val Leu Gly Gln Phe Asn Leu Gly Phe Ile Ile Ala Lys Leu
 705 710 715 720

Glu Arg Asp Leu Phe Ile Val Asp Gln His Ala Ala Asp Glu Lys Phe
 725 730 735

Asn Phe Glu His Leu Ala Arg Ser Thr Val Leu Asn Gln Gln Pro Leu
 740 745 750

Leu Gln Pro Leu Asn Leu Glu Leu Ser Pro Glu Glu Glu Val Thr Val
 755 760 765

Leu Met His Met Asp Ile Ile Arg Glu Asn Gly Phe Leu Leu Glu Glu
 770 775 780

Asn Pro Ser Ala Pro Pro Gly Lys His Phe Arg Leu Arg Ala Ile Pro
 785 790 795 800

Tyr Ser Lys Asn Ile Thr Phe Gly Val Glu Asp Leu Lys Asp Leu Ile
 805 810 815

Ser Thr Leu Gly Asp Asn His Gly Glu Cys Ser Val Ala Ser Ser Tyr
 820 825 830

Lys Thr Ser Lys Thr Asp Ser Ile Cys Pro Ser Arg Val Arg Ala Met
 835 840 845

Leu Ala Ser Arg Ala Cys Arg Ser Ser Val Met Ile Gly Asp Pro Leu
 850 855 860

Arg Lys Asn Glu Met Gln Lys Ile Val Glu His Leu Ala Asp Leu Glu
 865 870 875 880

Ser Pro Trp Asn Cys Pro His Gly Arg Pro Thr Met Arg His Leu Val
 885 890 895

Asp Leu Thr Thr Leu Leu Thr Leu Pro Asp Asp Asp Asn Val Asn Asp
 900 905 910

Asp Asp Asp Asp Asp Ala Thr Ile Ser Leu Ala
 915 920

<210> 41
 <211> 3466
 <212> DNA
 <213> Arabidopsis thaliana

<400> 41
 ttcgaattct ctcagctcaa aacatcgttt ctctctcact ctctctcaca attccaaaaa 60
 atgcagcgcc agagatcgat tttgtctttc ttccaaaaac ccacggcggc gactacgaag 120
 ggtttggttt cggcgatgc tgctagcggc gggggcggca gcggaggacc acgatttaat 180
 gtgaaggaag gggatgctaa aggcgacgct tctgtacgtt ttgctgtttc gaaatctgtc 240
 gatgagggtta gaggaacgga tactccaccg gagaaggttc cgcgtcgtgt cctgccgtct 300
 ggatttaagc cggctgaatc cgccggtgat gcttcgtccc tgttctccaa tattatgcat 360
 aagtttgtaa aagtcgatga tcgagattgt tctggagaga ggagccgaga agatgttggt 420
 ccgctgaatg attcatctct atgtatgaag gctaataatg ttattcctca atttcgttcc 480
 aataatggta aaactcaaga aagaaacat gcttttagtt tcagtgggag agctgaactt 540
 agatcagtag aagatatagg agtagatggc gatgttcctg gtccagaaac accagggatg 600
 cgtccacgtg cttctcgctt gaagcgagtt ctggaggatg aaatgacttt taaggaggat 660

MOR0251.ST25.txt

aagggttcctg	tattggactc	taacaaaagg	ctgaaaatgc	tccaggatcc	ggtttgtgga	720
gagaagaaaag	aagtaaacga	aggaacccaa	tttgaatggc	ttgagtcttc	tcgaatcagg	780
gatgccaaata	gaagacgtcc	tgatgatccc	ctttacgata	gaaagacctt	acacatacca	840
cctgatgttt	tcaagaaaat	gtctgcatca	caaaagcaat	attggagtgt	taagagtga	900
tatatggaca	ttgtgctttt	ctttaaagt	gggaaatttt	atgagctgta	tgagctagat	960
gcggaattag	gtcacaagga	gcttgactgg	aagatgacca	tgagtgggtg	gggaaaatgc	1020
agacagggtg	gtatctctga	aagtgggata	gatgaggcag	tgcaaaagct	attagctcgt	1080
ggatataaaag	ttggacgaat	cgagcagcta	gaaacatctg	accaagcaaa	agccagaggt	1140
gctaatacta	taattccaag	gaagctagtt	caggtattaa	ctccatcaac	agcaagcgag	1200
ggaaacatcg	ggcctgatgc	cgctccatctt	cttgctataa	aagagatcaa	aatggagcta	1260
caaaagtgtt	caactgtgta	tggatttgct	tttgttgact	gtgctgcctt	gaggttttgg	1320
gttgggtcca	tcagcgatga	tgcacatgt	gctgctcttg	gagcgttatt	gatgcaggtt	1380
tctccaaagg	aagtgttata	tgacagtaaa	gggctatcaa	gagaagcaca	aaaggctcta	1440
aggaaatata	cgttgacagg	gtctacggcg	gtacagttgg	ctccagtacc	acaagtaatg	1500
ggggatacag	atgctgctgg	agttagaaat	ataatagaat	ctaacggata	ctttaaaggt	1560
tcttctgaat	catggaactg	tgctgttgat	ggtctaaatg	aatgtgatgt	tgcccttagt	1620
gctcttgagg	agctaattaa	tcatctgtct	aggctaaagc	tagaagatgt	acttaagcat	1680
ggggatatatt	ttccatacca	agtttacagg	ggttgctctca	gaattgatgg	ccagacgatg	1740
gtaaactcttg	agatatattaa	caatagctgt	gatgggtgcc	ttcagggacc	cttgaacaaa	1800
tatcttgaaa	actgtgttag	tccaactgg	aagcgactct	taaggaattg	gatctgccat	1860
ccactcaaag	atgtagaaa	catcaataaa	cggcttgatg	tagttgaaga	attcacggca	1920
aactcagaaa	gtatgcaaat	caactggccag	tatctccaca	aacttccaga	cttagaaaga	1980
ctgctcggac	gcatcaagtc	tagcgttcga	tcatcagcct	ctgtgttgcc	tgctcttctg	2040
gggaaaaaag	tgctgaaaca	acgagttaaa	gcatttgggc	aaattgtgaa	agggttcaga	2100
agtggaaattg	atctgttggt	ggctctacag	aaggaatcaa	atatgatgag	tttgctttat	2160
aaactctgta	aacttcctat	attagtagga	aaaagcgggc	tagagttatt	tctttctcaa	2220
ttcgaagcag	ccatagatag	cgactttcca	aattatcaga	accaagatgt	gacagatgaa	2280
aacgctgaaa	ctctcacaat	acttatcgaa	ctttttatcg	aaagagcaac	tcaatggtct	2340
gaggtcattc	acaccataag	ctgcctagat	gtcctgagat	cttttgcaat	cgcagcaagt	2400
ctctctgctg	gaagcatggc	caggcctggt	atttttcccg	aatcagaagc	tacagatcag	2460
aatcagaaaa	caaaagggcc	aataactaaa	atccaaggac	tatggcatcc	atttgcagtt	2520
gcagccgatg	gtcaattgcc	tgttccgaat	gatatactcc	ttggcgaggc	tagaagaagc	2580
agtggcagca	ttcatcctcg	gtcattgtta	ctgacgggac	caaacatggg	cggaaaaatca	2640
actcttcttc	gtgcaacatg	tctggccggt	atctttgccc	aacttggctg	ctacgtgccg	2700
tgtgagtctt	gcgaaatctc	cctcgtggat	actatcttca	caaggcttgg	cgcacatgat	2760

MOR0251.ST25.txt

agaatcatga caggagagag tacctttttg gtagaatgca ctgagacagc gtcagttctt 2820
 cagaatgcaa ctgaggattc actagtaatc cttgacgaac tgggcagagg aactagtact 2880
 ttcgatggat acgccattgc atactcgggtt ttctcgtcacc tggtagagaa agttcaatgt 2940
 cggatgctct ttgcaacaca ttaccaccct ctaccaagg aattcgcgtc tcaccacgt 3000
 gtcacctcga aacacatggc ttgcgcattc aaatcaagat ctgattatca accacgtggt 3060
 tgtgatcaag acctagtgtt cttgtaccgt ttaaccgagg gagcttgtcc tgagagctac 3120
 ggacttcaag tggcactcat ggctggaata ccaaaccaag tggttgaaac agcatcaggt 3180
 gctgctcaag ccatgaagag atcaattggg gaaaacttca agtcaagtga gctaagatct 3240
 gagttctcaa gtctgcatga agactggctc aagtcattgg tgggtatttc tcgagtcgcc 3300
 cacaacaatg ccccatgttg cgaagatgac tacgacactt tgttttgctt atggcatgag 3360
 atcaaatcct cttactgtgt tcccaaataa atggctatga cataacacta tctgaagctc 3420
 gttaagtctt ttgcttctct gatgtttatt cctcttaaaa aatgcg 3466

<210> 42
 <211> 1109
 <212> PRT
 <213> Arabidopsis thaliana

<400> 42

Met Gln Arg Gln Arg Ser Ile Leu Ser Phe Phe Gln Lys Pro Thr Ala
 1 5 10 15

Ala Thr Thr Lys Gly Leu Val Ser Gly Asp Ala Ala Ser Gly Gly Gly
 20 25 30

Gly Ser Gly Gly Pro Arg Phe Asn Val Lys Glu Gly Asp Ala Lys Gly
 35 40 45

Asp Ala Ser Val Arg Phe Ala Val Ser Lys Ser Val Asp Glu Val Arg
 50 55 60

Gly Thr Asp Thr Pro Pro Glu Lys Val Pro Arg Arg Val Leu Pro Ser
 65 70 75 80

Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp Ala Ser Ser Leu Phe Ser
 85 90 95

Asn Ile Met His Lys Phe Val Lys Val Asp Asp Arg Asp Cys Ser Gly
 100 105 110

Glu Arg Ser Arg Glu Asp Val Val Pro Leu Asn Asp Ser Ser Leu Cys
 115 120 125

Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys
 130 135 140

Thr Gln Glu Arg Asn His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu
 145 150 155 160

Arg Ser Val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu
 165 170 175
 Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu
 180 185 190
 Asp Glu Met Thr Phe Lys Glu Asp Lys Val Pro Val Leu Asp Ser Asn
 195 200 205
 Lys Arg Leu Lys Met Leu Gln Asp Pro Val Cys Gly Glu Lys Lys Glu
 210 215 220
 Val Asn Glu Gly Thr Lys Phe Glu Trp Leu Glu Ser Ser Arg Ile Arg
 225 230 235 240
 Asp Ala Asn Arg Arg Arg Pro Asp Asp Pro Leu Tyr Asp Arg Lys Thr
 245 250 255
 Leu His Ile Pro Pro Asp Val Phe Lys Lys Met Ser Ala Ser Gln Lys
 260 265 270
 Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met Asp Ile Val Leu Phe Phe
 275 280 285
 Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu Leu Asp Ala Glu Leu Gly
 290 295 300
 His Lys Glu Leu Asp Trp Lys Met Thr Met Ser Gly Val Gly Lys Cys
 305 310 315 320
 Arg Gln Val Gly Ile Ser Glu Ser Gly Ile Asp Glu Ala Val Gln Lys
 325 330 335
 Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg Ile Glu Gln Leu Glu Thr
 340 345 350
 Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn Thr Ile Ile Pro Arg Lys
 355 360 365
 Leu Val Gln Val Leu Thr Pro Ser Thr Ala Ser Glu Gly Asn Ile Gly
 370 375 380
 Pro Asp Ala Val His Leu Leu Ala Ile Lys Glu Ile Lys Met Glu Leu
 385 390 395 400
 Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala Phe Val Asp Cys Ala Ala
 405 410 415
 Leu Arg Phe Trp Val Gly Ser Ile Ser Asp Asp Ala Ser Cys Ala Ala
 420 425 430

MOR0251.ST25.txt

Leu Gly Ala Leu Leu Met Gln Val Ser Pro Lys Glu Val Leu Tyr Asp
 435 440 445
 Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys Ala Leu Arg Lys Tyr Thr
 450 455 460
 Leu Thr Gly Ser Thr Ala Val Gln Leu Ala Pro Val Pro Gln Val Met
 465 470 475 480
 Gly Asp Thr Asp Ala Ala Gly Val Arg Asn Ile Ile Glu Ser Asn Gly
 485 490 495
 Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn Cys Ala Val Asp Gly Leu
 500 505 510
 Asn Glu Cys Asp Val Ala Leu Ser Ala Leu Gly Glu Leu Ile Asn His
 515 520 525
 Leu Ser Arg Leu Lys Leu Glu Asp Val Leu Lys His Gly Asp Ile Phe
 530 535 540
 Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg Ile Asp Gly Gln Thr Met
 545 550 555 560
 Val Asn Leu Glu Ile Phe Asn Asn Ser Cys Asp Gly Val Leu Gln Gly
 565 570 575
 Pro Leu Asn Lys Tyr Leu Glu Asn Cys Val Ser Pro Thr Gly Lys Arg
 580 585 590
 Leu Leu Arg Asn Trp Ile Cys His Pro Leu Lys Asp Val Glu Ser Ile
 595 600 605
 Asn Lys Arg Leu Asp Val Val Glu Glu Phe Thr Ala Asn Ser Glu Ser
 610 615 620
 Met Gln Ile Thr Gly Gln Tyr Leu His Lys Leu Pro Asp Leu Glu Arg
 625 630 635 640
 Leu Leu Gly Arg Ile Lys Ser Ser Val Arg Ser Ser Ala Ser Val Leu
 645 650 655
 Pro Ala Leu Leu Gly Lys Lys Val Leu Lys Gln Arg Val Lys Ala Phe
 660 665 670
 Gly Gln Ile Val Lys Gly Phe Arg Ser Gly Ile Asp Leu Leu Leu Ala
 675 680 685
 Leu Gln Lys Glu Ser Asn Met Met Ser Leu Leu Tyr Lys Leu Cys Lys
 690 695 700
 Leu Pro Ile Leu Val Gly Lys Ser Gly Leu Glu Leu Phe Leu Ser Gln
 705 710 715 720

Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro Asn Tyr Gln Asn Gln Asp
 725 730 735
 Val Thr Asp Glu Asn Ala Glu Thr Leu Thr Ile Leu Ile Glu Leu Phe
 740 745 750
 Ile Glu Arg Ala Thr Gln Trp Ser Glu Val Ile His Thr Ile Ser Cys
 755 760 765
 Leu Asp Val Leu Arg Ser Phe Ala Ile Ala Ala Ser Leu Ser Ala Gly
 770 775 780
 Ser Met Ala Arg Pro Val Ile Phe Pro Glu Ser Glu Ala Thr Asp Gln
 785 790 795 800
 Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys Ile Gln Gly Leu Trp His
 805 810 815
 Pro Phe Ala Val Ala Ala Asp Gly Gln Leu Pro Val Pro Asn Asp Ile
 820 825 830
 Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly Ser Ile His Pro Arg Ser
 835 840 845
 Leu Leu Leu Thr Gly Pro Asn Met Gly Gly Lys Ser Thr Leu Leu Arg
 850 855 860
 Ala Thr Cys Leu Ala Val Ile Phe Ala Gln Leu Gly Cys Tyr Val Pro
 865 870 875 880
 Cys Glu Ser Cys Glu Ile Ser Leu Val Asp Thr Ile Phe Thr Arg Leu
 885 890 895
 Gly Ala Ser Asp Arg Ile Met Thr Gly Glu Ser Thr Phe Leu Val Glu
 900 905 910
 Cys Thr Glu Thr Ala Ser Val Leu Gln Asn Ala Thr Gln Asp Ser Leu
 915 920 925
 Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr Phe Asp Gly Tyr
 930 935 940
 Ala Ile Ala Tyr Ser Val Phe Arg His Leu Val Glu Lys Val Gln Cys
 945 950 955 960
 Arg Met Leu Phe Ala Thr His Tyr His Pro Leu Thr Lys Glu Phe Ala
 965 970 975
 Ser His Pro Arg Val Thr Ser Lys His Met Ala Cys Ala Phe Lys Ser
 980 985 990

Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp Gln Asp Leu Val Phe Leu
 995 1000 1005

Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu Ser Tyr Gly Leu Gln
 1010 1015 1020

Val Ala Leu Met Ala Gly Ile Pro Asn Gln Val Val Glu Thr Ala
 1025 1030 1035

Ser Gly Ala Ala Gln Ala Met Lys Arg Ser Ile Gly Glu Asn Phe
 1040 1045 1050

Lys Ser Ser Glu Leu Arg Ser Glu Phe Ser Ser Leu His Glu Asp
 1055 1060 1065

Trp Leu Lys Ser Leu Val Gly Ile Ser Arg Val Ala His Asn Asn
 1070 1075 1080

Ala Pro Ile Gly Glu Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp
 1085 1090 1095

His Glu Ile Lys Ser Ser Tyr Cys Val Pro Lys
 1100 1105

<210> 43
 <211> 5307
 <212> DNA
 <213> Arabidopsis thaliana

<400> 43
 aaagataagt tcatacgact tttgtggctc atcaaaggcc atcatcgctc tctatataca 60
 atttagtgct ttatagtaca aaaccttcca ctccctttg tccaaagttt tccaatttaa 120
 tttataaaca ggaataatat tatctatata ataaagtga aaataactat cattgtccaa 180
 ataatttggc cgttgatcat gttactacaa agaaatgaaa tccttagtag aagtatatat 240
 atatatatat ttgtaacaca ctcaaatgg taggtgttgt tacagacaga tgttcgtag 300
 cccagtaagc ccaatatgag atttaatggg ccttgatatt ttatagacca aacattgaaa 360
 cattgcacgc ctggtctcaa agaacgttaa tacacgcgcc gccggttgcc gccaatccgc 420
 tttcccgcca aattcgacac cataaatttc ttctagtcgc ttctgattcc agttccactg 480
 aaaaaccacg aaagaagaac atttgcaccg tagttgcaga aggtagggtga aggatttagc 540
 tttctctatc ttccaatgga gggtaatttc gaggaacaga acaagcttcc ggagctgaaa 600
 ttgggtaatg ttaaacccta gttttttttt tctttctcat ttctgtattc gatttcccaa 660
 ttgggtttat ggggttttga aaagggtctga tatttggtat gcattttttt tttaattttt 720
 ggaagatgca aagcaagctc aagggtttct ctcgttctac aaaaccctac caaatgtaag 780
 ttctcgtttt ctttcgattt ctgggagaag tttagagcttg tacagtgcct ctaattgcaa 840
 taaataacac caattctagt cggaaagtag atgctttaaa attagggttt gaagcaattg 900
 tagacatttt gttcattggg aagcgaatta ggaaaaaagg cttaagattt tttagcaatt 960

MOR0251.ST25.txt

tctcgatctt	tgcttatgtg	ggttttgatt	gttctttgct	tcaggatacg	agagctgtta	1020
gattcttttga	tcgcaaggtg	agttcattgt	tctcaaattg	tctagacttt	ggttgtttaa	1080
atgtcgtcat	tgatttatgg	aaatTTTTTg	aatgcatttg	caggattatt	atacagctca	1140
tggtgaaaat	tcagttttca	ttgcaaagac	ttattatcat	acaaccactg	ctctacgtca	1200
gctcgggagt	ggttcaaattg	ctctttcaag	cgtaagcatt	agtaggaaca	tgttcgaaac	1260
gattgctagg	gatcttctcc	tgagagcgtg	tgatcatact	gtagaacttt	atgaaggaag	1320
cggatcgaat	tgagagacttg	tgaaaacagg	ttctcctgga	aacattggaa	gctttgaaga	1380
tgttttgttt	gcaaacaattg	aaatgcagga	cacaccagtt	gttgtctcca	tatttccaag	1440
ttttcacgat	ggcagatgcg	ttattgggat	ggcctatggt	gatctgacta	ggcgagttct	1500
tggtactagct	gagtttcttg	atgatagccg	cttcaccaat	ctggagtctt	cgttgattgc	1560
tctaggcgca	aaagaatgca	tttttccagc	tgaatccggc	aaatccaatg	aatgcaaaaag	1620
cctgtatgat	tccttgagga	gggtgtgccgt	gatgataaca	gagaggaaga	aacacgagtt	1680
caaaggaaga	gatttagatt	cagatcttaa	gagattgggt	aaggggaata	ttgagcctgt	1740
tagagatttg	gtatccgggt	ttgaccttgc	gactcctgct	ctaggtgcat	tactctcggt	1800
ttctgaactt	ctctcaaatg	aggataacta	tggaacttcc	acaatccgca	gatatgatat	1860
tggtcgattc	atgagacttg	actctgcagc	tatgagggcg	ttgaatgtga	tggtgagcaa	1920
aactgatgct	aataagaatt	tcagtttggt	tggtctcatg	aacagaacat	gtaccgcagg	1980
gatgggtaag	agactgcttc	atatgtggct	gaagcaaccc	ctcgtggatt	tgaatgagat	2040
taagacgaga	ttagatatag	ttcagtgcct	tggtgaagaa	gctgggttaa	ggcaggatct	2100
tagacagcat	ctgaagcgaa	tctcagatgt	tgagaggctt	ttgcgcagtc	tcgagagaag	2160
aagaggtggg	ttacagcaca	ttattaaact	ctatcaggta	ctttccgcac	ttcaatctgc	2220
ttctctcaat	gttaacaaaa	ttgcattttc	attgtcctaa	atgtgtttat	gcaactctga	2280
agttataggt	atgttattaa	gttcattact	aattaagtct	tcattctttc	tctgcagtca	2340
gctataaggc	ttcccttcat	caaaacagct	atgcaacagt	acaccggaga	attcgcatca	2400
ctcatcagcg	agaggtacct	gaaaaagctt	gaggctttat	cagatcaaga	tcaccttgga	2460
aagttcatcg	atttggttga	gtgctctgta	gatcttgacc	agctagaaaa	tggtgagaatac	2520
atgatatctt	caaactacga	caccaaattg	gcattctctga	aagatcagaa	agaattgctg	2580
gagcagcaga	ttcacgaatt	gcacaaaaag	acagcgatag	aacttgatct	tcaggtcgac	2640
aaggctctta	aacttgacaa	agcagcgcaa	tttgggcatg	tcttcaggat	cacgaagaag	2700
gaagagccaa	agatcaggaa	gaagctgacg	acacagttta	tagtgctgga	gactcgcaaa	2760
gacggagtga	agttcacaaa	cacaaagcta	aaaaaactgg	gcgaccagta	ccaaagtgtt	2820
gtggatgatt	ataggagctg	tcaaaaggag	ctcgttgatc	gtgtagttga	gactgttacc	2880
agcttctctg	aggtatgttt	agttattcat	attaagcatt	ggactgttac	agaattgggt	2940
gtttaaaaatc	atagtaaaact	atatgtggaa	tttatatgta	tattgtatgg	ttataggtat	3000
ttgaggactt	agctgggtta	ctttctgaaa	tggtatgttt	gttaagcttt	gctgatttgg	3060

ctgccagttg	ccctactcca	tactgtaggc	cagaaatcac	ctctttgggt	agtacaatct	3120
caagttgatt	attttgttct	gaaaatgaat	agttttttct	ttccaagttt	atgacataat	3180
gttgagagca	cggttaataa	attgtaggat	gctggagata	ttgtactaga	aggaagcaga	3240
catccatgtg	tagaagctca	agattgggtg	aatttcatac	caaagattg	cagactcgta	3300
agtattgaat	gtggtaaata	aactgagacg	tctttgtttt	tcttgtttcc	cttttgactt	3360
gaacaaatac	ttgtttgccc	tttactgttc	tttgaaatca	gatgagaggg	aagagttggt	3420
ttcaaatagt	aacagggcct	aacatgggag	ggaagtcac	tttcatccgc	caggtatgat	3480
gatttcctct	agttcagttt	tgttcatag	acgtatgact	aaagtcgggt	tccggccatt	3540
ataaatccca	ggttggtgtg	attgtgctga	tggtcaagt	tggttccttt	gttccttgtg	3600
ataaagcatc	aatttccata	agagactgca	tctttgcccg	tgtaggagca	ggcgattgcc	3660
aagtgaagttt	aagtttagcc	ctcaatgaac	gaaaaactgc	tgatatcctg	aacaccctta	3720
ttccaacttt	ttttcctttg	gtgtgttagc	tgcgtggagt	gtcaactttt	atgcaagaaa	3780
tgcttgaaac	cgcatcgata	ttgaaaggcg	ctactgataa	gtcactgata	attatcgatg	3840
aacttggtcg	tggaacatca	acttatgatg	gttttggtta	gtttctctgc	aatttctctt	3900
ctttcatttg	gatgttttta	gtaagttttc	tattatatat	tcatttttat	ggcatatatgt	3960
gagatttcag	tgctcttgac	atcatcgtgg	tgaatatatc	aggttttagct	tgggctatat	4020
gtgagcatct	ggttcaagtg	aaaagagcac	caactctggt	tgctactcac	ttccatgaac	4080
ttactgcctt	ggctcaagca	aactctgagg	tctctggtaa	cactgttggt	gtggcaaact	4140
tccatgtcag	cgctcacatt	gacactgaaa	gccgcaaact	caccatgctt	tacaaggctc	4200
ggtttataaa	ttaaaaaatt	gctgatctgt	tgcaagttaa	agtgtctctg	tttttatggt	4260
taatctaaat	tacttatttg	attttcttac	aaagatgaaa	ttgaaattaa	ttttgtgtgg	4320
tgtgttgttt	gtctgggttag	gttgaaccag	gggcctgtga	ccagagcttt	gggattcatg	4380
tggcggaatt	tgccaacttc	cctgaaagcg	tcgtggccct	cgcaagagag	aaagctgcag	4440
agctggaaga	tttctctccc	tctcgtatga	taatcaacaa	tgaggtcttg	attcatttcc	4500
ccctttgttt	ttggttgatg	atggaatcat	tctatcattc	acccattctg	cagtttatgc	4560
tatattatta	taaatctatg	tgacaaagat	ttaattctcg	tattgttggt	tgcaaggagag	4620
tgggaagaga	aagagcagag	aagatgatcc	agatgaagta	tcaagagggg	cagagcgagc	4680
tcacaagttt	ctgaaagagt	ttgcagcgat	gccacttgat	aaaatggagc	ttaaagattc	4740
acttcaacgg	gtacgtgaga	tgaaagatga	gctagagaaa	gatgctgcag	actgccactg	4800
gctcaggcag	tttctgtgaa	gaaccctga	cgttttttgg	tttttggttt	tgtaaatagc	4860
ttaaatcggg	tctttagatt	gtggtcgttg	cttgggatga	aactaaatga	gggcaaaaac	4920
ataattctac	attttttgtt	agtaaagctc	gttaattttac	tccctagtgc	tatcaattat	4980
tttgccctatt	ataattgttg	atcaagtact	tagagcaacc	ccaatgggtt	ctaaacataa	5040
gtttcttatt	ttatagagag	aaatttttatt	ataaaaaaat	gtgtgggttt	cttgatttagt	5100
gaagaaacca	tctccaaaat	accttatatt	cttatataag	gtatttttga	gagaattttct	5160

MOR0251.ST25.txt

aactattcaa gaaacttaca taattaaata ctattatttt tattgtttta atgttaagaa 5220
 acttatattt aaaaaccacc aatggaattg ctcttagcta ccatacaaat aattataaaa 5280
 atatatcgaa aagtagaaga gccattt 5307

<210> 44
 <211> 937
 <212> PRT
 <213> Arabidopsis thaliana

<400> 44

Met Glu Gly Asn Phe Glu Glu Gln Asn Lys Leu Pro Glu Leu Lys Leu
 1 5 10 15

Asp Ala Lys Gln Ala Gln Gly Phe Leu Ser Phe Tyr Lys Thr Leu Pro
 20 25 30

Asn Asp Thr Arg Ala Val Arg Phe Phe Asp Arg Lys Asp Tyr Tyr Thr
 35 40 45

Ala His Gly Glu Asn Ser Val Phe Ile Ala Lys Thr Tyr Tyr His Thr
 50 55 60

Thr Thr Ala Leu Arg Gln Leu Gly Ser Gly Ser Asn Ala Leu Ser Ser
 65 70 75 80

Val Ser Ile Ser Arg Asn Met Phe Glu Thr Ile Ala Arg Asp Leu Leu
 85 90 95

Leu Glu Arg Asn Asp His Thr Val Glu Leu Tyr Glu Gly Ser Gly Ser
 100 105 110

Asn Trp Arg Leu Val Lys Thr Gly Ser Pro Gly Asn Ile Gly Ser Phe
 115 120 125

Glu Asp Val Leu Phe Ala Asn Asn Glu Met Gln Asp Thr Pro Val Val
 130 135 140

Val Ser Ile Phe Pro Ser Phe His Asp Gly Arg Cys Val Ile Gly Met
 145 150 155 160

Ala Tyr Val Asp Leu Thr Arg Arg Val Leu Gly Leu Ala Glu Phe Leu
 165 170 175

Asp Asp Ser Arg Phe Thr Asn Leu Glu Ser Ser Leu Ile Ala Leu Gly
 180 185 190

Ala Lys Glu Cys Ile Phe Pro Ala Glu Ser Gly Lys Ser Asn Glu Cys
 195 200 205

Lys Ser Leu Tyr Asp Ser Leu Glu Arg Cys Ala Val Met Ile Thr Glu
 210 215 220

MOR0251.ST25.txt

Arg Lys Lys His Glu Phe Lys Gly Arg Asp Leu Asp Ser Asp Leu Lys
 225 230 235 240

Arg Leu Val Lys Gly Asn Ile Glu Pro Val Arg Asp Leu Val Ser Gly
 245 250 255

Phe Asp Leu Ala Thr Pro Ala Leu Gly Ala Leu Leu Ser Phe Ser Glu
 260 265 270

Leu Leu Ser Asn Glu Asp Asn Tyr Gly Asn Phe Thr Ile Arg Arg Tyr
 275 280 285

Asp Ile Gly Gly Phe Met Arg Leu Asp Ser Ala Ala Met Arg Ala Leu
 290 295 300

Asn Val Met Glu Ser Lys Thr Asp Ala Asn Lys Asn Phe Ser Leu Phe
 305 310 315 320

Gly Leu Met Asn Arg Thr Cys Thr Ala Gly Met Gly Lys Arg Leu Leu
 325 330 335

His Met Trp Leu Lys Gln Pro Leu Val Asp Leu Asn Glu Ile Lys Thr
 340 345 350

Arg Leu Asp Ile Val Gln Cys Phe Val Glu Glu Ala Gly Leu Arg Gln
 355 360 365

Asp Leu Arg Gln His Leu Lys Arg Ile Ser Asp Val Glu Arg Leu Leu
 370 375 380

Arg Ser Leu Glu Arg Arg Arg Gly Gly Leu Gln His Ile Ile Lys Leu
 385 390 395 400

Tyr Gln Ser Ala Ile Arg Leu Pro Phe Ile Lys Thr Ala Met Gln Gln
 405 410 415

Tyr Thr Gly Glu Phe Ala Ser Leu Ile Ser Glu Arg Tyr Leu Lys Lys
 420 425 430

Leu Glu Ala Leu Ser Asp Gln Asp His Leu Gly Lys Phe Ile Asp Leu
 435 440 445

Val Glu Cys Ser Val Asp Leu Asp Gln Leu Glu Asn Gly Glu Tyr Met
 450 455 460

Ile Ser Ser Asn Tyr Asp Thr Lys Leu Ala Ser Leu Lys Asp Gln Lys
 465 470 475 480

Glu Leu Leu Glu Gln Gln Ile His Glu Leu His Lys Lys Thr Ala Ile
 485 490 495

Glu Leu Asp Leu Gln Val Asp Lys Ala Leu Lys Leu Asp Lys Ala Ala
 500 505 510

Gln Phe Gly His Val Phe Arg Ile Thr Lys Lys Glu Glu Pro Lys Ile
 515 520 525
 Arg Lys Lys Leu Thr Thr Gln Phe Ile Val Leu Glu Thr Arg Lys Asp
 530 535 540
 Gly Val Lys Phe Thr Asn Thr Lys Leu Lys Lys Leu Gly Asp Gln Tyr
 545 550 555 560
 Gln Ser Val Val Asp Asp Tyr Arg Ser Cys Gln Lys Glu Leu Val Asp
 565 570 575
 Arg Val Val Glu Thr Val Thr Ser Phe Ser Glu Val Phe Glu Asp Leu
 580 585 590
 Ala Gly Leu Leu Ser Glu Met Asp Val Leu Leu Ser Phe Ala Asp Leu
 595 600 605
 Ala Ala Ser Cys Pro Thr Pro Tyr Cys Arg Pro Glu Ile Thr Ser Leu
 610 615 620
 Asp Ala Gly Asp Ile Val Leu Glu Gly Ser Arg His Pro Cys Val Glu
 625 630 635 640
 Ala Gln Asp Trp Val Asn Phe Ile Pro Asn Asp Cys Arg Leu Met Arg
 645 650 655
 Gly Lys Ser Trp Phe Gln Ile Val Thr Gly Pro Asn Met Gly Gly Lys
 660 665 670
 Ser Thr Phe Ile Arg Gln Val Gly Val Ile Val Leu Met Ala Gln Val
 675 680 685
 Gly Ser Phe Val Pro Cys Asp Lys Ala Ser Ile Ser Ile Arg Asp Cys
 690 695 700
 Ile Phe Ala Arg Val Gly Ala Gly Asp Cys Gln Leu Arg Gly Val Ser
 705 710 715 720
 Thr Phe Met Gln Glu Met Leu Glu Thr Ala Ser Ile Leu Lys Gly Ala
 725 730 735
 Thr Asp Lys Ser Leu Ile Ile Ile Asp Glu Leu Gly Arg Gly Thr Ser
 740 745 750
 Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Cys Glu His Leu Val
 755 760 765
 Gln Val Lys Arg Ala Pro Thr Leu Phe Ala Thr His Phe His Glu Leu
 770 775 780

MOR0251.ST25.txt

Thr Ala Leu Ala Gln Ala Asn Ser Glu Val Ser Gly Asn Thr Val Gly
785 790 795 800

Val Ala Asn Phe His Val Ser Ala His Ile Asp Thr Glu Ser Arg Lys
805 810 815

Leu Thr Met Leu Tyr Lys Val Glu Pro Gly Ala Cys Asp Gln Ser Phe
820 825 830

Gly Ile His Val Ala Glu Phe Ala Asn Phe Pro Glu Ser Val Val Ala
835 840 845

Leu Ala Arg Glu Lys Ala Ala Glu Leu Glu Asp Phe Ser Pro Ser Ser
850 855 860

Met Ile Ile Asn Asn Glu Glu Ser Gly Lys Arg Lys Ser Arg Glu Asp
865 870 875 880

Asp Pro Asp Glu Val Ser Arg Gly Ala Glu Arg Ala His Lys Phe Leu
885 890 895

Lys Glu Phe Ala Ala Met Pro Leu Asp Lys Met Glu Leu Lys Asp Ser
900 905 910

Leu Gln Arg Val Arg Glu Met Lys Asp Glu Leu Glu Lys Asp Ala Ala
915 920 925

Asp Cys His Trp Leu Arg Gln Phe Leu
930 935

<210> 45
<211> 3521
<212> DNA
<213> Arabidopsis thaliana

<400> 45
ctaagaaagc ggcgaaaaat tggcaaccca agttcgccat agccacgacc acgaccttcc 60
atttctctta aacggaggag attacgaata aagcaattat gggcaagcaa aagcagcaga 120
cgatttctcg tttcttcgct cccaaaccca aatccccgac tcacgaaccg aatccggtag 180
ccgaatcatc aacaccgcca ccgaagatat ccgccactgt atccttctct cttccaagc 240
gtaagcttct ctccgaccac ctgcgcgccg cgtcacccaa aaagcctaaa ctttctctc 300
acactcaaaa ccagtagacc gatcccaatt tacaccaaag atttctccag agatttctgg 360
aacctcgcg ggaggaatat gttcccgaaa cgatcatcag gaggaatac acaccattgg 420
aacagcaagt ggtggagcta aagagcaagt acccagatgt ggttttgatg gtggaagttg 480
gttacaggta cagattcttc ggagaagacg cggagatcgc agcacgcgtg ttgggtat 540
acgctcatat ggatcacaat ttcattgacg cgagtgtgcc aacatttcga ttgaatttcc 600
atgtgagaag actggtgaat gcaggatata agattggtgt agtgaagcag actgaaactg 660
cagccattaa gtcccatggt gcaaaccgga ccggcccttt tttccgggga ctgtcggcgt 720

MOR0251.ST25.txt

tgtataccaa agccacgctt gaagcggctg aggatataag tgggtggtgt ggtggtgaag	780
aaggtttttg ttcacagagt aatttcttgg tttgtgttgt ggatgagaga gttaagtcgg	840
agacattagg ctgtggtatt gaaatgagtt ttgatgttag agtcggtgtt gttggcgttg	900
aaatttcgac aggtgaagtt gtttatgaag agttcaatga taatttcacg agaagtggat	960
tagaggctgt gattttgagc ttgtcaccag ctgagctgtt gcttggccag cctctttcac	1020
aacaaactga gaagtttttg gtggcacatg ctggacctac ctcaaactgt cgagtgaac	1080
gtgcctcact ggattgtttc agcaatggta atgcagtaga tgaggttatt tcattatgtg	1140
aaaaaatcag cgcaggtaac ttagaagatg ataaagaaat gaagctggag gctgctgaaa	1200
aaggaatgct ttgcttgaca gttcatacaa ttatgaacat gccacatctg actgttcaag	1260
ccctcgccct aacgttttgc catctcaaac agtttggatt tgaaaggatc ctttaccag	1320
gggcctcatt tcgctctttg tcaagtaaca cagagatgac tctctcagcc aatactctgc	1380
aacagttgga ggttgtgaaa aataattcag atggatcgga atctggctcc ttattccata	1440
atatgaatca cacacttaca gtatatggtt ccaggcttct tagacactgg gtgactcatc	1500
ctctatgcga tagaaatttg atatctgctc ggcttgatgc tgtttctgag atttctgctt	1560
gcatgggac tcatagttct tcccagctca gcagtgaagt ggttgaagaa ggttctgaga	1620
gagcaattgt atcacctgag ttttatctcg tgctctctc agtcttgaca gctatgtcta	1680
gatcatctga tattcaacgt ggaataacaa gaatctttca tcggactgct aaagccacag	1740
agttcattgc agttatgga gctattttac ttgcggggaa gcaaattcag cggcttgga	1800
taaagcaaga ctctgaaatg aggagtatgc aatctgcaac tgtgcgatct actcttttga	1860
gaaaattgat ttctgttatt tcatccctg ttgtggttga caatgccgga aaacttctct	1920
ctgccctaaa taaggaagcg gctgttcgag gtgacttgct cgacatacta atcacttcca	1980
gcgaccaatt tcctgagctt gctgaagctc gccaaagcgt tttagtcac agggaaaagc	2040
tggattctc gatagcttca tttcgcaaga agctcgctat tcgaaatttg gaatttcttc	2100
aagtgtcggg gatcacacat ttgatagagc tgcccgttga ttccaaggct cctatgaatt	2160
gggtgaaagt aaatagcacc aagaagacta ttcgatatca tccccagaa atagtagctg	2220
gcttgatga gctagctcta gcaactgaac atcttgccat tgtgaaccga gcttcgtggg	2280
atagtttct caagagtttc agtagatact acacagattt taaggctgcc gttcaagctc	2340
ttgctgcact ggactgtttg cactcccttt caactctatc tagaaacaag aactatgtcc	2400
gtcccagatt tgtggatgac tgtgaaccag ttgagataaa catacagtct ggtcgtcatc	2460
ctgtactgga gactatatta caagataact tcgtcccaaa tgacacaatt ttgcatgcag	2520
aaggggaata ttgccaaatt atcaccggac ctaacatggg aggaaagagc tgctatatcc	2580
gtcaagttgc tttaatttcc ataattggctc aggttggttc ctttgtacca gcgtcattcg	2640
ccaagctgca cgtgcttgat ggtgttttca ctcggatggg tgcttcagac agtatccagc	2700
atggcagaag taccttttca gaagaattaa gtgaagcgtc acacataatc agaacctgtt	2760
cttctcgttc gcttggtata ttagatgagc ttggaagagg cactagcaca cagcaggtg	2820

MOR0251.ST25.txt

```

tagccattgc ctatgcaaca ttacagcatc tcctagcaga aaagagatgt ttggttcttt 2880
ttgtcacgca ttaccctgaa atagctgaga tcagtaacgg attcccaggt tctggttgga 2940
cataccatgt ctcgatatctg acattgcaga aggataaagg cagttatgat catgatgatg 3000
tgacctacct atataagctt gtgcgtggtc tttgcagcag gagctttggg tttaagggtg 3060
ctcagcttgc ccagatacct ccatcatgta tacgtcgagc catttcaatg gctgcaaaat 3120
tggaagctga ggtacgtgca agagagagaa atacacgcat gggagaacca gaaggacatg 3180
aagaaccgag aggcgcagaa gaatctatct cggtcttagg tgacttggtt gcagacctga 3240
aatttgctct ctctgaagag gacccttgga aagcattcga gtttttaaag catgcttgga 3300
agattgctgg caaaatcaga ctaaaaccaa cttgttcatt ttgatttaat cttaacatta 3360
tagcaactgc aaggtcttga tcatctgtta gttgcgtact aacttatgtg tattagtata 3420
acaagaaaag agaattagag agatggattc taatccggtg ttgcagtaca tcttttctcc 3480
accgcataa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 3521

```

```

<210> 46
<211> 1081
<212> PRT
<213> Arabidopsis thaliana

```

```
<400> 46
```

```
Met Gly Lys Gln Lys Gln Gln Thr Ile Ser Arg Phe Phe Ala Pro Lys
1          5          10          15
```

```
Pro Lys Ser Pro Thr His Glu Pro Asn Pro Val Ala Glu Ser Ser Thr
20          25          30
```

```
Pro Pro Pro Lys Ile Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg
35          40          45
```

```
Lys Leu Leu Ser Asp His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys
50          55          60
```

```
Leu Ser Pro His Thr Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln
65          70          75          80
```

```
Arg Phe Leu Gln Arg Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro
85          90          95
```

```
Glu Thr Ser Ser Ser Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val
100         105         110
```

```
Glu Leu Lys Ser Lys Tyr Pro Asp Val Val Leu Met Val Glu Val Gly
115         120         125
```

```
Tyr Arg Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile Ala Ala Arg Val
130         135         140
```

```
Leu Gly Ile Tyr Ala His Met Asp His Asn Phe Met Thr Ala Ser Val
145         150         155         160
```

Pro Thr Phe Arg Leu Asn Phe His Val Arg Arg Leu Val Asn Ala Gly
 165 170 175
 Tyr Lys Ile Gly Val Val Lys Gln Thr Glu Thr Ala Ala Ile Lys Ser
 180 185 190
 His Gly Ala Asn Arg Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu
 195 200 205
 Tyr Thr Lys Ala Thr Leu Glu Ala Ala Glu Asp Ile Ser Gly Gly Cys
 210 215 220
 Gly Gly Glu Glu Gly Phe Gly Ser Gln Ser Asn Phe Leu Val Cys Val
 225 230 235 240
 Val Asp Glu Arg Val Lys Ser Glu Thr Leu Gly Cys Gly Ile Glu Met
 245 250 255
 Ser Phe Asp Val Arg Val Gly Val Val Gly Val Glu Ile Ser Thr Gly
 260 265 270
 Glu Val Val Tyr Glu Glu Phe Asn Asp Asn Phe Met Arg Ser Gly Leu
 275 280 285
 Glu Ala Val Ile Leu Ser Leu Ser Pro Ala Glu Leu Leu Leu Gly Gln
 290 295 300
 Pro Leu Ser Gln Gln Thr Glu Lys Phe Leu Val Ala His Ala Gly Pro
 305 310 315 320
 Thr Ser Asn Val Arg Val Glu Arg Ala Ser Leu Asp Cys Phe Ser Asn
 325 330 335
 Gly Asn Ala Val Asp Glu Val Ile Ser Leu Cys Glu Lys Ile Ser Ala
 340 345 350
 Gly Asn Leu Glu Asp Asp Lys Glu Met Lys Leu Glu Ala Ala Glu Lys
 355 360 365
 Gly Met Ser Cys Leu Thr Val His Thr Ile Met Asn Met Pro His Leu
 370 375 380
 Thr Val Gln Ala Leu Ala Leu Thr Phe Cys His Leu Lys Gln Phe Gly
 385 390 395 400
 Phe Glu Arg Ile Leu Tyr Gln Gly Ala Ser Phe Arg Ser Leu Ser Ser
 405 410 415
 Asn Thr Glu Met Thr Leu Ser Ala Asn Thr Leu Gln Gln Leu Glu Val
 420 425 430

MOR0251.ST25.txt

Val Lys Asn Asn Ser Asp Gly Ser Glu Ser Gly Ser Leu Phe His Asn
 435 440 445

Met Asn His Thr Leu Thr Val Tyr Gly Ser Arg Leu Leu Arg His Trp
 450 455 460

Val Thr His Pro Leu Cys Asp Arg Asn Leu Ile Ser Ala Arg Leu Asp
 465 470 475 480

Ala Val Ser Glu Ile Ser Ala Cys Met Gly Ser His Ser Ser Ser Gln
 485 490 495

Leu Ser Ser Glu Leu Val Glu Glu Gly Ser Glu Arg Ala Ile Val Ser
 500 505 510

Pro Glu Phe Tyr Leu Val Leu Ser Ser Val Leu Thr Ala Met Ser Arg
 515 520 525

Ser Ser Asp Ile Gln Arg Gly Ile Thr Arg Ile Phe His Arg Thr Ala
 530 535 540

Lys Ala Thr Glu Phe Ile Ala Val Met Glu Ala Ile Leu Leu Ala Gly
 545 550 555 560

Lys Gln Ile Gln Arg Leu Gly Ile Lys Gln Asp Ser Glu Met Arg Ser
 565 570 575

Met Gln Ser Ala Thr Val Arg Ser Thr Leu Leu Arg Lys Leu Ile Ser
 580 585 590

Val Ile Ser Ser Pro Val Val Val Asp Asn Ala Gly Lys Leu Leu Ser
 595 600 605

Ala Leu Asn Lys Glu Ala Ala Val Arg Gly Asp Leu Leu Asp Ile Leu
 610 615 620

Ile Thr Ser Ser Asp Gln Phe Pro Glu Leu Ala Glu Ala Arg Gln Ala
 625 630 635 640

Val Leu Val Ile Arg Glu Lys Leu Asp Ser Ser Ile Ala Ser Phe Arg
 645 650 655

Lys Lys Leu Ala Ile Arg Asn Leu Glu Phe Leu Gln Val Ser Gly Ile
 660 665 670

Thr His Leu Ile Glu Leu Pro Val Asp Ser Lys Val Pro Met Asn Trp
 675 680 685

Val Lys Val Asn Ser Thr Lys Lys Thr Ile Arg Tyr His Pro Pro Glu
 690 695 700

Ile Val Ala Gly Leu Asp Glu Leu Ala Leu Ala Thr Glu His Leu Ala
 705 710 715 720

```

Ile Val Asn Arg Ala Ser Trp Asp Ser Phe Leu Lys Ser Phe Ser Arg
      725                      730                      735

Tyr Tyr Thr Asp Phe Lys Ala Ala Val Gln Ala Leu Ala Ala Leu Asp
      740                      745                      750

Cys Leu His Ser Leu Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg
      755                      760                      765

Pro Glu Phe Val Asp Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser
      770                      775                      780

Gly Arg His Pro Val Leu Glu Thr Ile Leu Gln Asp Asn Phe Val Pro
      785                      790                      795                      800

Asn Asp Thr Ile Leu His Ala Glu Gly Glu Tyr Cys Gln Ile Ile Thr
      805                      810                      815

Gly Pro Asn Met Gly Gly Lys Ser Cys Tyr Ile Arg Gln Val Ala Leu
      820                      825                      830

Ile Ser Ile Met Ala Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala
      835                      840                      845

Lys Leu His Val Leu Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp
      850                      855                      860

Ser Ile Gln His Gly Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala
      865                      870                      875                      880

Ser His Ile Ile Arg Thr Cys Ser Ser Arg Ser Leu Val Ile Leu Asp
      885                      890                      895

Glu Leu Gly Arg Gly Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr
      900                      905                      910

Ala Thr Leu Gln His Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe
      915                      920                      925

Val Thr His Tyr Pro Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly
      930                      935                      940

Ser Val Gly Thr Tyr His Val Ser Tyr Leu Thr Leu Gln Lys Asp Lys
      945                      950                      955                      960

Gly Ser Tyr Asp His Asp Asp Val Thr Tyr Leu Tyr Lys Leu Val Arg
      965                      970                      975

Gly Leu Cys Ser Arg Ser Phe Gly Phe Lys Val Ala Gln Leu Ala Gln
      980                      985                      990

```


MOR0251.ST25.txt

Ile Pro Pro Ser Cys Ile Arg Arg Ala Ile Ser Met Ala Ala Lys Leu
 995 1000 1005

Glu Ala Glu Val Arg Ala Arg Glu Arg Asn Thr Arg Met Gly Glu
 1010 1015 1020

Pro Glu Gly His Glu Glu Pro Arg Gly Ala Glu Glu Ser Ile Ser
 1025 1030 1035

Ala Leu Gly Asp Leu Phe Ala Asp Leu Lys Phe Ala Leu Ser Glu
 1040 1045 1050

Glu Asp Pro Trp Lys Ala Phe Glu Phe Leu Lys His Ala Trp Lys
 1055 1060 1065

Ile Ala Gly Lys Ile Arg Leu Lys Pro Thr Cys Ser Phe
 1070 1075 1080

<210> 47
 <211> 7080
 <212> DNA
 <213> Arabidopsis thaliana

<400> 47
 ctcttcgccg actgtttcac tccccttctc tctcactctc tgtgcgcttt attccactct 60
 ccgatggctc cgtctcgccg acagatcagc ggaagatctc cgttggtgaa ccagcagcgt 120
 caaatcacct ccttcttttg gaaatctgct tcatcatctt cttctccgtc tccatctcct 180
 tcaccatctc tctccaataa gaaaaccccc aaatctaaca accctaacc taaatctccg 240
 tctccgtcac catctccgcc taagaaaacc cccaaattga accctaacc tagttctaata 300
 cttcctgctc gtagtcctag ccctggctct gatactcctt ctctgtgaca gtccaagttt 360
 aagaagcccc ttctcgtcat cggacagaca ctttcgcctc ctcaatcggg ggtaattact 420
 tacggtgacg aggtgggtgg gaagcaagtt aggggtttatt ggcctttgga taaaaaatgg 480
 tatgatggga gcgtgacgtt ttatgataag ggtgagggtg agcatgtggt tgagtatgaa 540
 gatggggaag aagagtcttt ggatttgga aaggagaaga ctgagtgggt ggttggggaa 600
 aaatcaggag ataggtttaa tcgattgaaa cgaggcgctt cggctttgag aaaagttgtg 660
 acggatagtg atgatgatgt ggagatgggt aatgtggaag aagataaaag tgacggtgat 720
 gattctagcg atgaggattg gggaaagaat gttgggaagg aggtttgtga gagtgaagaa 780
 gatgatgtgg agttggttga tgagaatgaa atggatgaag aagagttggt ggaagagaaa 840
 gatgaagaaa cttctaaagt taatagagta tccaaaactg actctagaaa gcggaagact 900
 agtgaagtaa cgaaatcagg tggtgagaag aaaagcaaga ctgatacagg cactatcttg 960
 aaaggtttta aggcttctgt tgtggagcct gcgaagaaga ttggacaagg taaaccgaag 1020
 agtctcttgt tgtaatcata tgcttgattt tgcattgttt tagtttggg tatgtctctt 1080
 gcactgactt ttgtttcaga tagtgtatgt tgttggttgc ttaatatatt ttgtgtctta 1140
 ctacagctga taggggtggtc aagggttttg aagataacgt gttggatggg gatgctcttg 1200

MOR0251.ST25.txt

ctagatttgg tgctcgtgat tctgagaaat tccgcttttt gggagtgtaa gtctttcaca	1260
aaaaaaattc catcttagag gctatttgct acggtgggta ggagtagaga atgtaaattt	1320
gtgtcttaag caatattgac ttctctactg gcaggagcat ctctggtttt cttttatctt	1380
catgatgtat tagtaggctg catgatccct attctagcta agttagttct gttaattatt	1440
tttgggtaac agagaccgaa gggatgctaa aaggagacgc cctactgatg agaattatga	1500
tccgaggaca ctctacctcc ctctgattt tgtgaaaaa ttaactggag gccaggtcag	1560
aagagcgcac ggaaatctgg ttcaggattt ttggtgaagc taatcaactt tcacttatat	1620
gattttgtgg ctttttttca gagacaatgg tgggagttta aagcaaagca tatggacaaa	1680
gttgatttct tcaaggtaga acgataatta cttatttcgt tataacttat ttattgatgg	1740
gagattctag gataaatggt cttcttttgt ggcaagcaga tgggtaaatt ctatgagctt	1800
tttgagatgg atgcacatgt cggagctaag gaactggata tacaatacat gaaggtaact	1860
gtttgttatg actcataact aggtgatgca tttgaagaca tctgttaaaa atgttaaaaa	1920
accgaaaatt tggcatcaga ttatgctaaa agggttcttt tcattgggtgt tacattacaa	1980
atttctctcg tattgtctct aatgtatctc tctttacaag cccctgacat atgcatttat	2040
tttgtaggga gagcaacctc attgtggatt tccggagaag aatttttctg taaacattga	2100
gaaattagtt agaaaggttt gtttccagaa atatagcaac tccagttcaa gcgtgatcta	2160
tttcttggtt cgtgtagaga aattacattc atggcaaagc ctgtactttg ggtagaaata	2220
aagttgattg aattgaatgg aacagggcta tcgggtttta gttgtcgaaac aaacagaaac	2280
acctgatcag ctggagcaac gccgaaaaga gacaggttcc aaggataaag tatgtccac	2340
tatgaatcta atttagttgg cattatcagt tcaagtcaat ttgtttgctc ttgaaactaa	2400
aatttgttca ctttggtgta tgcctatgta gaaaaattat gatagggagg gctcatagt	2460
acagaacttc tgtttttata ggttggtgaag cgcaagtat gtgcagttgt taaaaaggc	2520
acgctgacag atggggagat gctattaact aatccggatg catcttatct aatggccttg	2580
actgaaggag gagaaagttt aactaatcct acagcagagc acaattttgg tgtatgtttg	2640
gttgatgttg cgacacagaa gataatactg ggccagggtga gttctagttg atgaatggta	2700
cctggttgca cttatacgta acatttctcg gtgtatattg atggcatttt tttttcattc	2760
gtaccagttt aaggatgatc aagattgcag tgcattatct tgcctgctat ctgagatgag	2820
gccggtggaa attattaaac cagctaaggt gttgagttat gcaacagaga gaacaatagt	2880
tagacaaaacc agaaatccct tagtaaataa tctcgttcca ctttctgaat tttgggatcc	2940
ggagaagacc atatatgaag ttggaattat ctacaagcga atcaattgtc aaccgtcttc	3000
tgcttattct agtgagggaa agattctagg tgatggttca agctttcttc caaaaatgtt	3060
gtctgaatta gcaactgaag ataagaatgg tagcctggca ctctctgctc ttggtgggtgc	3120
catttactac ctgcgacaag cattcttgga tgagagtctg cttagatttg caaagtttga	3180
atccctgcct tactgtgatt tcagcaacgt taatgagaag cagcacatgg ttcttgatgc	3240
tgctgctctt gaaaaccttg agatatattga aaacagtaga aatggaggct attcagggtg	3300

aagtttctct atcttaccat gtattattaa acataattga tgtgttctaa atctagagtg	3360
ttgtcttttg aagaacgctg tatgctcaac tgaatcaatg tatcactgca tctgggaaac	3420
ggttactgaa aacatggctg gcaagacctt tatataatac ggaactgac aaggaacgac	3480
aagatgctgt agcaattctg cgggtgagtc tttcaacaag ttgtttgact ttgctgctgt	3540
catttctctg tctctcaact agacaataac ttggcatctt ggtttcacat ttgatcattt	3600
ttcatgtctg ttctgctatc catggatctc tcttcagaat tacactatct cccattatg	3660
ggtgttcaag accatttttg ccaactgtttc actggcaaag atgatgtttt cctatgcgtt	3720
caactaacca tctattttcta gaacttattc cctaagatta taaaacttac tctgcttctt	3780
cagcatgtca aggctttcgt ttacactatc catctgacaa tgtattatgg tactgtccct	3840
tccctcaggg tgaaaatctt ccgtactcac tggaattccg gaagtcggtg tccagacttc	3900
cagacatgga acggttgatt gcacgtatgt tttctagcat gtaagggtt agctagattg	3960
agatgttaat tcttacatta tatgtttata ccaaagactt actaaacata tttgttaaac	4020
ttgtgttacg tgttatagtg aagctagtgg aagaaatggc gataaagtgg tgctatatga	4080
agatacagct aagaagcagg tacaggaatt catatcaact ctacgtgggt gtgaaacaat	4140
ggcagaagca tgctcttctc tccgtgctat cttgaagcat gatacatcca ggcggtgct	4200
tcatttacta actcctggta taatcaattt gctccatatt cacattctta tactggcaaa	4260
ttgcacagca tctcatatca tttctctgcc aggtcaaagt cttccaaata tatcatctc	4320
cataaagtat ttcaaggatg cttttgactg ggtagaagct cacaattctg gacgtgtaat	4380
accccatgaa ggagcagatg aagagtatga ttgtgcctgc aaaacagtag aagaatttga	4440
gtccagtttg aaaaaacatc tgaaagagca acggaaatta ctcgagatg catcagtgag	4500
aattacttca ctattttttt ttactcctta aatggctaata caaccgaggg ttttctgac	4560
agatcttttg tgctcttttg tcttcttctc cagataaact atgttacagt tggaaaagat	4620
gaatacctct tggaagttcc tgaaagttha agtgggagtg ttctcatga ttatgaatta	4680
tgctcatcga aaaaggtaaa agttgtacca agtttcacat tctaaagaaa ttggcatttc	4740
gcttctgca taacaagtcg atagtcttct cgtaattgct gtctgctgat atatttacta	4800
tatagagacc cttaatttta aacatgagat tttcttactt ttactctct ttcagggtgt	4860
ctctcgatat tggactccta ccataaagaa attattaaaa gagctatcac aagcaaaatc	4920
tgaaaaagag tcggccctga agagcatttc acagagattg attggacgtt tctgcgagca	4980
tcaagaaaaa tggagacaat tggtttctgc aacagctggt atggacaagt tcatgtttta	5040
aaaaaaaaa attgtttaag gaattttcag catcttcctt cagaatatgt atcttgctta	5100
tccaattcct gttaattact gtcaccagct gttagctttg tgggtcgtcg cttggaccct	5160
tttctgttg aacatttggt gagctagtta gaattgagtt tgatcccaca ctttatagat	5220
tgagttagaa gtaggcagtc agaagaaaat gaattctagg cagacgtata gttcaatcac	5280
atcttataag caagaggttt cttgggtgga agattgtttt atagaattag gcatgcaaac	5340
aactttgcac ttagacctt atgtggatc atttttgaca tgaattcttt ctattgcaga	5400

MOR0251.ST25.txt

gctggacgtg ttgatcagcc tcgcttttgc aagtgattct tatgaaggag taagatgccg 5460
 cccagtaata tctggttcta catctgatgg tggtccacac ttgtctgcc ctggtctagg 5520
 gcatccagtt ctaaggggtg attcgtagg cagaggctct tttgtaccaa ataattgtaaa 5580
 gataggtggt gctgagaaa ccagtttcat cctcctcaca ggcctaata tgggtggaaa 5640
 atcaaccctt cttcgccaag tttgcttggc tgtaattctg gctcaggtaa gctatcattt 5700
 gaaaaaactt tgtaggcaat gggctttgac ccgtttaatt ttgatgaaag aaactcaagc 5760
 aatgatgatc ttttcacaga ttggagcaga tgtcccagca gaaacctttg aggtttcgcc 5820
 tggtgacaaa atttgtgtcc ggatgggtgc aaaagatcat atcatggcag gacaaagcac 5880
 gtttttaaca gaactttcag aaactgcggt aatgttggtg agtaatgttc attctgtttg 5940
 tcaaattgat tacatgaagc tttctaagat aaatgtgaaa cttgccacag tggttaccct 6000
 tttgagagtt ggtcacaggc tttgttaaac tatgcgaatg ccaacaaacg cactgataga 6060
 atgttttata ttaataatat gcagacatca gccacccgaa actcgctggt ggtgctagat 6120
 gagcttgac gaggaacagc cacatcagat gggcaagcca ttgcgtatgt tgaatcaatt 6180
 attgcgtatc atgttttttg ggacttactg ttattgttca ctttatctaa aatatcttaa 6240
 ctatttacag ggaatccgta cttgagcact tcatagaaaa ggtgcagtgt agaggattct 6300
 tctctactca ttatcatcgt ctctctgtgg attatcaaac caatccaaag gtattgtgaa 6360
 aagtgtctgc ttcagtttct gggtttgaaa gacttgagaa ctatcaataa taatctgatt 6420
 gtttgtgtac attctgaaac ttgtcaaaaa ccgatcagtc ttgaatattt gtttggatag 6480
 gtctcacttt gccatattgc atgtcaaata ggagaaggaa tcggtggagt agaagaagtt 6540
 acatttctct atagattgac tcctgggtga tgtcctaaaa gttatggagt taacgttgct 6600
 cggttagctg gtaagaacac tgaattctct actccatcac ctctactcag ttaaacagaa 6660
 gcagtcactc atcaaattgt tttggtttta atctccatag gtcttcaga ttacgtactc 6720
 cagagagccg tgataaaaac ccaagaattc gaggttttgt acggtaaaaa ccatagaaaa 6780
 accgatcata aattagcagc aatgataaag cagatcatca gcagtgttgc atcagattct 6840
 gattactcag cttcaaagga ctcatgtgt gagctacact ccatggccaa tacatttctc 6900
 cggttaacca actaattdaa cagctctacg cttttccggt ttgtcgttct tcttgtaact 6960
 ctttaaccaa ggtcaatcca cgagcttcgt cgtgtcaaat actaaaacct gagtcagcct 7020
 gaaactaaac tcctgagtag agactcagtt ttgaggtgtg ggtttagctt ctgagctttt 7080

<210> 48

<211> 1324

<212> PRT

<213> Arabidopsis thaliana

<400> 48

Met Ala Pro Ser Arg Arg Gln Ile Ser Gly Arg Ser Pro Leu Val Asn
 1 5 10 15

Gln Gln Arg Gln Ile Thr Ser Phe Phe Gly Lys Ser Ala Ser Ser Ser
 20 25 30

Ser Ser Pro Ser Pro Ser Pro Ser Pro Ser Leu Ser Asn Lys Lys Thr
 35 40 45
 Pro Lys Ser Asn Asn Pro Asn Pro Lys Ser Pro Ser Pro Ser Pro Ser
 50 55 60
 Pro Pro Lys Lys Thr Pro Lys Leu Asn Pro Asn Pro Ser Ser Asn Leu
 65 70 75 80
 Pro Ala Arg Ser Pro Ser Pro Gly Pro Asp Thr Pro Ser Pro Val Gln
 85 90 95
 Ser Lys Phe Lys Lys Pro Leu Leu Val Ile Gly Gln Thr Pro Ser Pro
 100 105 110
 Pro Gln Ser Val Val Ile Thr Tyr Gly Asp Glu Val Val Gly Lys Gln
 115 120 125
 Val Arg Val Tyr Trp Pro Leu Asp Lys Lys Trp Tyr Asp Gly Ser Val
 130 135 140
 Thr Phe Tyr Asp Lys Gly Glu Gly Lys His Val Val Glu Tyr Glu Asp
 145 150 155 160
 Gly Glu Glu Glu Ser Leu Asp Leu Gly Lys Glu Lys Thr Glu Trp Val
 165 170 175
 Val Gly Glu Lys Ser Gly Asp Arg Phe Asn Arg Leu Lys Arg Gly Ala
 180 185 190
 Ser Ala Leu Arg Lys Val Val Thr Asp Ser Asp Asp Asp Val Glu Met
 195 200 205
 Gly Asn Val Glu Glu Asp Lys Ser Asp Gly Asp Asp Ser Ser Asp Glu
 210 215 220
 Asp Trp Gly Lys Asn Val Gly Lys Glu Val Cys Glu Ser Glu Glu Asp
 225 230 235 240
 Asp Val Glu Leu Val Asp Glu Asn Glu Met Asp Glu Glu Glu Leu Val
 245 250 255
 Glu Glu Lys Asp Glu Glu Thr Ser Lys Val Asn Arg Val Ser Lys Thr
 260 265 270
 Asp Ser Arg Lys Arg Lys Thr Ser Glu Val Thr Lys Ser Gly Gly Glu
 275 280 285
 Lys Lys Ser Lys Thr Asp Thr Gly Thr Ile Leu Lys Gly Phe Lys Ala
 290 295 300

MOR0251.ST25.txt

Ser Val Val Glu Pro Ala Lys Lys Ile Gly Gln Ala Asp Arg Val Val
 305 310 315 320

Lys Gly Leu Glu Asp Asn Val Leu Asp Gly Asp Ala Leu Ala Arg Phe
 325 330 335

Gly Ala Arg Asp Ser Glu Lys Phe Arg Phe Leu Gly Val Asp Arg Arg
 340 345 350

Asp Ala Lys Arg Arg Arg Pro Thr Asp Glu Asn Tyr Asp Pro Arg Thr
 355 360 365

Leu Tyr Leu Pro Pro Asp Phe Val Lys Lys Leu Thr Gly Gly Gln Arg
 370 375 380

Gln Trp Trp Glu Phe Lys Ala Lys His Met Asp Lys Val Val Phe Phe
 385 390 395 400

Lys Met Gly Lys Phe Tyr Glu Leu Phe Glu Met Asp Ala His Val Gly
 405 410 415

Ala Lys Glu Leu Asp Ile Gln Tyr Met Lys Gly Glu Gln Pro His Cys
 420 425 430

Gly Phe Pro Glu Lys Asn Phe Ser Val Asn Ile Glu Lys Leu Val Arg
 435 440 445

Lys Gly Tyr Arg Val Leu Val Val Glu Gln Thr Glu Thr Pro Asp Gln
 450 455 460

Leu Glu Gln Arg Arg Lys Glu Thr Gly Ser Lys Asp Lys Val Val Lys
 465 470 475 480

Arg Glu Val Cys Ala Val Val Thr Lys Gly Thr Leu Thr Asp Gly Glu
 485 490 495

Met Leu Leu Thr Asn Pro Asp Ala Ser Tyr Leu Met Ala Leu Thr Glu
 500 505 510

Gly Gly Glu Ser Leu Thr Asn Pro Thr Ala Glu His Asn Phe Gly Val
 515 520 525

Cys Leu Val Asp Val Ala Thr Gln Lys Ile Ile Leu Gly Gln Phe Lys
 530 535 540

Asp Asp Gln Asp Cys Ser Ala Leu Ser Cys Leu Leu Ser Glu Met Arg
 545 550 555 560

Pro Val Glu Ile Ile Lys Pro Ala Lys Val Leu Ser Tyr Ala Thr Glu
 565 570 575

Arg Thr Ile Val Arg Gln Thr Arg Asn Pro Leu Val Asn Asn Leu Val
 580 585 590

Pro Leu Ser Glu Phe Trp Asp Ser Glu Lys Thr Ile Tyr Glu Val Gly
 595 600 605
 Ile Ile Tyr Lys Arg Ile Asn Cys Gln Pro Ser Ser Ala Tyr Ser Ser
 610 615 620
 Glu Gly Lys Ile Leu Gly Asp Gly Ser Ser Phe Leu Pro Lys Met Leu
 625 630 635 640
 Ser Glu Leu Ala Thr Glu Asp Lys Asn Gly Ser Leu Ala Leu Ser Ala
 645 650 655
 Leu Gly Gly Ala Ile Tyr Tyr Leu Arg Gln Ala Phe Leu Asp Glu Ser
 660 665 670
 Leu Leu Arg Phe Ala Lys Phe Glu Ser Leu Pro Tyr Cys Asp Phe Ser
 675 680 685
 Asn Val Asn Glu Lys Gln His Met Val Leu Asp Ala Ala Ala Leu Glu
 690 695 700
 Asn Leu Glu Ile Phe Glu Asn Ser Arg Asn Gly Gly Tyr Ser Gly Thr
 705 710 715 720
 Leu Tyr Ala Gln Leu Asn Gln Cys Ile Thr Ala Ser Gly Lys Arg Leu
 725 730 735
 Leu Lys Thr Trp Leu Ala Arg Pro Leu Tyr Asn Thr Glu Leu Ile Lys
 740 745 750
 Glu Arg Gln Asp Ala Val Ala Ile Leu Arg Gly Glu Asn Leu Pro Tyr
 755 760 765
 Ser Leu Glu Phe Arg Lys Ser Leu Ser Arg Leu Pro Asp Met Glu Arg
 770 775 780
 Leu Ile Ala Arg Met Phe Ser Ser Ile Glu Ala Ser Gly Arg Asn Gly
 785 790 795 800
 Asp Lys Val Val Leu Tyr Glu Asp Thr Ala Lys Lys Gln Val Gln Glu
 805 810 815
 Phe Ile Ser Thr Leu Arg Gly Cys Glu Thr Met Ala Glu Ala Cys Ser
 820 825 830
 Ser Leu Arg Ala Ile Leu Lys His Asp Thr Ser Arg Arg Leu Leu His
 835 840 845
 Leu Leu Thr Pro Gly Gln Ser Leu Pro Asn Ile Ser Ser Ser Ile Lys
 850 855 860

MOR0251.ST25.txt

Tyr Phe Lys Asp Ala Phe Asp Trp Val Glu Ala His Asn Ser Gly Arg
 865 870 875 880

Val Ile Pro His Glu Gly Ala Asp Glu Glu Tyr Asp Cys Ala Cys Lys
 885 890 895

Thr Val Glu Glu Phe Glu Ser Ser Leu Lys Lys His Leu Lys Glu Gln
 900 905 910

Arg Lys Leu Leu Gly Asp Ala Ser Ile Asn Tyr Val Thr Val Gly Lys
 915 920 925

Asp Glu Tyr Leu Leu Glu Val Pro Glu Ser Leu Ser Gly Ser Val Pro
 930 935 940

His Asp Tyr Glu Leu Cys Ser Ser Lys Lys Gly Val Ser Arg Tyr Trp
 945 950 955 960

Thr Pro Thr Ile Lys Lys Leu Leu Lys Glu Leu Ser Gln Ala Lys Ser
 965 970 975

Glu Lys Glu Ser Ala Leu Lys Ser Ile Ser Gln Arg Leu Ile Gly Arg
 980 985 990

Phe Cys Glu His Gln Glu Lys Trp Arg Gln Leu Val Ser Ala Thr Ala
 995 1000 1005

Glu Leu Asp Val Leu Ile Ser Leu Ala Phe Ala Ser Asp Ser Tyr
 1010 1015 1020

Glu Gly Val Arg Cys Arg Pro Val Ile Ser Gly Ser Thr Ser Asp
 1025 1030 1035

Gly Val Pro His Leu Ser Ala Thr Gly Leu Gly His Pro Val Leu
 1040 1045 1050

Arg Gly Asp Ser Leu Gly Arg Gly Ser Phe Val Pro Asn Asn Val
 1055 1060 1065

Lys Ile Gly Gly Ala Glu Lys Ala Ser Phe Ile Leu Leu Thr Gly
 1070 1075 1080

Pro Asn Met Gly Gly Lys Ser Thr Leu Leu Arg Gln Val Cys Leu
 1085 1090 1095

Ala Val Ile Leu Ala Gln Ile Gly Ala Asp Val Pro Ala Glu Thr
 1100 1105 1110

Phe Glu Val Ser Pro Val Asp Lys Ile Cys Val Arg Met Gly Ala
 1115 1120 1125

Lys Asp His Ile Met Ala Gly Gln Ser Thr Phe Leu Thr Glu Leu
 1130 1135 1140

Ser Glu Thr Ala Val Met Leu Thr Ser Ala Thr Arg Asn Ser Leu
 1145 1150 1155
 Val Val Leu Asp Glu Leu Gly Arg Gly Thr Ala Thr Ser Asp Gly
 1160 1165 1170
 Gln Ala Ile Ala Glu Ser Val Leu Glu His Phe Ile Glu Lys Val
 1175 1180 1185
 Gln Cys Arg Gly Phe Phe Ser Thr His Tyr His Arg Leu Ser Val
 1190 1195 1200
 Asp Tyr Gln Thr Asn Pro Lys Val Ser Leu Cys His Met Ala Cys
 1205 1210 1215
 Gln Ile Gly Glu Gly Ile Gly Gly Val Glu Glu Val Thr Phe Leu
 1220 1225 1230
 Tyr Arg Leu Thr Pro Gly Ala Cys Pro Lys Ser Tyr Gly Val Asn
 1235 1240 1245
 Val Ala Arg Leu Ala Gly Leu Pro Asp Tyr Val Leu Gln Arg Ala
 1250 1255 1260
 Val Ile Lys Ser Gln Glu Phe Glu Ala Leu Tyr Gly Lys Asn His
 1265 1270 1275
 Arg Lys Thr Asp His Lys Leu Ala Ala Met Ile Lys Gln Ile Ile
 1280 1285 1290
 Ser Ser Val Ala Ser Asp Ser Asp Tyr Ser Ala Ser Lys Asp Ser
 1295 1300 1305
 Leu Cys Glu Leu His Ser Met Ala Asn Thr Phe Leu Arg Leu Thr
 1310 1315 1320

Asn

<210> 49
 <211> 2501
 <212> DNA
 <213> Oryza sativa

<400> 49
 cggcaccgaga ttttgcagtc tcctctcctc ctccgctcga gcgagtgagt cccgaccacg 60
 tcgctgccct cgcctcaccg ccggccaacc gccgtgacga gagatcgagc agggcggggc 120
 atggacgagc cttcgccgcg cggaggtggg tgccgctggg agccgccccg catccggagg 180
 ttggaggagt cggtggtgaa ccgcatcgcg gcgggggagg tgatccagcg gccgtcgtcg 240
 gcggtgaagg agctcatcga gaacagcctc gacgctggcg cctccagcgt ctccgttgcg 300

MOR0251.ST25.txt

gtgaaggacg gtggcctcaa gctcatccag gtctccgatg acggccatgg catcaggttt	360
gaggatttgg caatattgtg cgaaaggcat actacctcaa agttatctgc atacgaggat	420
ctgcagacca taaaatcgat ggggttcaga ggggaggctt tggctagtat gacttatgtt	480
ggccatgtta ccgtgacaac gataacagaa ggccaattgc acggtacag ggtttcttac	540
agagatggtg taatggagaa tgagcctaag ccttgcgctg cggtgaaagg aactcaagtc	600
atggttgaaa atctatttta caacatggta gcccgcaaga aaacattgca gaactccaat	660
gatgactacc ccaagatcgt agacttcac agtcggtttg cagtccatca catcaacggt	720
accttctctt gcagaaagca tggagccaat agagcagatg ttcatagtgc aagtacatcc	780
tcaaggttag atgctatcag gagtgtctat ggggcttctg tcgttcgtga tctcatagaa	840
ataaaggttt catatgagga tgctgcagat tcaatcttca agatggatgg ttacatctca	900
aatgcaaatt atgtggcaaa gaagattaca atgattcttt tcataaatga taggcttgta	960
gactgtactg ctttgaaaag agctattgaa tttgtgtact ctgcaacatt gcctcaagca	1020
tccaaacctt tcatatacat gtccatacat cttccatcag aacacgtgga tgtaaatata	1080
caccaacca agaaagaggt tagccttttg aatcaagagc gtattattga aacaataaga	1140
aatgctattg aggaaaaact gatgaattct aatacaacca ggatattcca aactcaggca	1200
ttaaaacttat cagggattgc tcaagctaac ccacaaaagg ataaggtttc tgaggccagt	1260
atgggttctg gaacaaaatc tcaaaaaatt cctgtgagcc aaatggtcag aacagatcca	1320
cgcaatccat ctggaagatt gcacacctac tggcacgggc aatcttcaaa\ tcttgaaaag	1380
aaatttgatc ttgtatctgt aagaaatgtt gtaagatcaa ggagaaacca aaaagatgct	1440
ggtgatttgt caagccgtca tgagctcctt gtggaaatag attctagctt ccacctggc	1500
cttttgga ca ttgtcaagaa ctgcacatat gttggacttg ccgatgaagc ctttgctttg	1560
atacaacaca ataccgctt ataccttgta aatgtggtaa atattagtaa agaacttatg	1620
taccagcaag ctttgtgccg ttttggaac ttcaatgcta ttcagctcag tgaaccagct	1680
ccacttcagg agttgctggt gatggcactg aaagacgatg aattgatgag tgatgaaaag	1740
gatgatgaga aactggagat tgcagaagta aacactgaga tactaaaaga aaatgctgag	1800
atgattaatg agtacttttc tattcacatt gatcaagatg gcaaattgac aagacttcct	1860
gttgactg accagtacac cctgatatg gaccgtcttc cagaatttgt gttggcttta	1920
ggaaatgatg ttacttgga tgacgagaaa gagtgttca gaacagtagc ttctgctgta	1980
ggaaacttct atgcacttca tcccccaatc cttccaaatc catctgggaa tggcattcat	2040
ttatacaaga aaaatagaga ttcaatggct gatgaacatg ctgagaatga tctaataatca	2100
gatgaaaatg acgttgatca agaacttctt gcggaagcag aagcagcatg ggcccaacgt	2160
gagtggacca ttcagcatgt cttgtttcca tccatgcgac ttttctcaa gccccgaag	2220
tcaatggcaa cagatggaac gtttgtgcag gttgttctt tggagaaact ctacaagatt	2280
tttgaaagggt gttagctcat aagtgagaaa atgaaggcag agtaagatca tgattcatgg	2340
agtgtttttg aaaatgtgta taatttcacc gtattatgta ctttgatagt gtctgtagaa	2400

actgaagaaa gaaagatggc ttacttctg aattgaaagt taacgatgcc agcaattgta 2460

tattctgatc aaccaaaaaa aaaaaaaaaa aaaaaaaaaa a 2501

<210> 50

<211> 724

<212> PRT

<213> Oryza sativa

<400> 50

Met Asp Glu Pro Ser Pro Arg Gly Gly Gly Cys Ala Gly Glu Pro Pro
1 5 10 15

Arg Ile Arg Arg Leu Glu Glu Ser Val Val Asn Arg Ile Ala Ala Gly
20 25 30

Glu Val Ile Gln Arg Pro Ser Ser Ala Val Lys Glu Leu Ile Glu Asn
35 40 45

Ser Leu Asp Ala Gly Ala Ser Ser Val Ser Val Ala Val Lys Asp Gly
50 55 60

Gly Leu Lys Leu Ile Gln Val Ser Asp Asp Gly His Gly Ile Arg Phe
65 70 75 80

Glu Asp Leu Ala Ile Leu Cys Glu Arg His Thr Thr Ser Lys Leu Ser
85 90 95

Ala Tyr Glu Asp Leu Gln Thr Ile Lys Ser Met Gly Phe Arg Gly Glu
100 105 110

Ala Leu Ala Ser Met Thr Tyr Val Gly His Val Thr Val Thr Thr Ile
115 120 125

Thr Glu Gly Gln Leu His Gly Tyr Arg Val Ser Tyr Arg Asp Gly Val
130 135 140

Met Glu Asn Glu Pro Lys Pro Cys Ala Ala Val Lys Gly Thr Gln Val
145 150 155 160

Met Val Glu Asn Leu Phe Tyr Asn Met Val Ala Arg Lys Lys Thr Leu
165 170 175

Gln Asn Ser Asn Asp Asp Tyr Pro Lys Ile Val Asp Phe Ile Ser Arg
180 185 190

Phe Ala Val His His Ile Asn Val Thr Phe Ser Cys Arg Lys His Gly
195 200 205

Ala Asn Arg Ala Asp Val His Ser Ala Ser Thr Ser Ser Arg Leu Asp
210 215 220

Ala Ile Arg Ser Val Tyr Gly Ala Ser Val Val Arg Asp Leu Ile Glu
225 230 235 240

```

Ile Lys Val Ser Tyr Glu Asp Ala Ala Asp Ser Ile Phe Lys Met Asp
      245                      250          255

Gly Tyr Ile Ser Asn Ala Asn Tyr Val Ala Lys Lys Ile Thr Met Ile
      260                      265          270

Leu Phe Ile Asn Asp Arg Leu Val Asp Cys Thr Ala Leu Lys Arg Ala
      275                      280          285

Ile Glu Phe Val Tyr Ser Ala Thr Leu Pro Gln Ala Ser Lys Pro Phe
      290                      295          300

Ile Tyr Met Ser Ile His Leu Pro Ser Glu His Val Asp Val Asn Ile
305                      310          315          320

His Pro Thr Lys Lys Glu Val Ser Leu Leu Asn Gln Glu Arg Ile Ile
      325                      330          335

Glu Thr Ile Arg Asn Ala Ile Glu Glu Lys Leu Met Asn Ser Asn Thr
      340                      345          350

Thr Arg Ile Phe Gln Thr Gln Ala Leu Asn Leu Ser Gly Ile Ala Gln
      355                      360          365

Ala Asn Pro Gln Lys Asp Lys Val Ser Glu Ala Ser Met Gly Ser Gly
      370                      375          380

Thr Lys Ser Gln Lys Ile Pro Val Ser Gln Met Val Arg Thr Asp Pro
385                      390          395          400

Arg Asn Pro Ser Gly Arg Leu His Thr Tyr Trp His Gly Gln Ser Ser
      405                      410          415

Asn Leu Glu Lys Lys Phe Asp Leu Val Ser Val Arg Asn Val Val Arg
      420                      425          430

Ser Arg Arg Asn Gln Lys Asp Ala Gly Asp Leu Ser Ser Arg His Glu
      435                      440          445

Leu Leu Val Glu Ile Asp Ser Ser Phe His Pro Gly Leu Leu Asp Ile
      450                      455          460

Val Lys Asn Cys Thr Tyr Val Gly Leu Ala Asp Glu Ala Phe Ala Leu
465                      470          475          480

Ile Gln His Asn Thr Arg Leu Tyr Leu Val Asn Val Val Asn Ile Ser
      485                      490          495

Lys Glu Leu Met Tyr Gln Gln Ala Leu Cys Arg Phe Gly Asn Phe Asn
      500                      505          510

```

MOR0251.ST25.txt

Ala Ile Gln Leu Ser Glu Pro Ala Pro Leu Gln Glu Leu Leu Val Met
 515 520 525

Ala Leu Lys Asp Asp Glu Leu Met Ser Asp Glu Lys Asp Asp Glu Lys
 530 535 540

Leu Glu Ile Ala Glu Val Asn Thr Glu Ile Leu Lys Glu Asn Ala Glu
 545 550 555 560

Met Ile Asn Glu Tyr Phe Ser Ile His Ile Asp Gln Asp Gly Lys Leu
 565 570 575

Thr Arg Leu Pro Val Val Leu Asp Gln Tyr Thr Pro Asp Met Asp Arg
 580 585 590

Leu Pro Glu Phe Val Leu Ala Leu Gly Asn Asp Val Thr Trp Asp Asp
 595 600 605

Glu Lys Glu Cys Phe Arg Thr Val Ala Ser Ala Val Gly Asn Phe Tyr
 610 615 620

Ala Leu His Pro Pro Ile Leu Pro Asn Pro Ser Gly Asn Gly Ile His
 625 630 635 640

Leu Tyr Lys Lys Asn Arg Asp Ser Met Ala Asp Glu His Ala Glu Asn
 645 650 655

Asp Leu Ile Ser Asp Glu Asn Asp Val Asp Gln Glu Leu Leu Ala Glu
 660 665 670

Ala Glu Ala Ala Trp Ala Gln Arg Glu Trp Thr Ile Gln His Val Leu
 675 680 685

Phe Pro Ser Met Arg Leu Phe Leu Lys Pro Pro Lys Ser Met Ala Thr
 690 695 700

Asp Gly Thr Phe Val Gln Val Ala Ser Leu Glu Lys Leu Tyr Lys Ile
 705 710 715 720

Phe Glu Arg Cys